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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

a	C							Result No.		
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153.6	155.2	155.2	692.2	741.2	1725.8	1725.8	1729	Score		
o O	9.0	9.0	40.0	42.9	99.8	99.8	100.0	Query e Match Length DB ID	фP	
4291	9985	2708	710	1833	52498	20052	1729	Length		
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0C928034	EADSPAB	U94513	PSU16119	AF037983	AF232004	AF232006	AF005221	DB ID		CHINAMUC
a minima Ocaranaa	Y13831 Erwinia amy	U94513 Erwinia amy	U16119 Pseudomonas	AF037983 Pseudomon	AF232004 Pseudomon	Af232006 Pseudomon	AF005221 Pseudomon	Description		

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MEDLINE
REFERENCE
AUTHORS
TITLE
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ORGANISM
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AF005221
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                                                                                                                                                                        KEYWORDS
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                                                    JOURNAL
                                                                                        JOURNAL
                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                      Submitted Ithaca, NY
                                                                                       The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate J. Bacteriol 180 (19), 5211-5217 (1998)
                                                           Direct Submission
                                                                  Charkowski, A.O.,
                                                                                                                           1 (bases 1 to 1729)
Charkowski, A.O., Alfano, J.R.,
                                                                                                                                                                              AF005221
AF005221.1
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Pseudomonas syringae hrp-secreted
                                                                                                                      Collmer, A.
                                                                                                                                                 Pseudomonas syringae
Bacteria; Proteobacteria;
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                                                                         (bases 1 to 1729)
                                            ed (23-MAY-1997) Plant
NY 14853, USA
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              /organism="Pseudomonas
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                                                                                                                           Preston, G.,
                                                   Pathology, Cornell University,
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                                                                                                                                                  Pseudomonadaceae;
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AC09388 Drosophil
AE003763 Drosophil
AB011839 Bacillus
Y07752 V carteri m
U62676 Halobacteri
AE005080 Halobacteri
AE005080 Chlamydom
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AC091196 Homo sapi
AL021999 Mycobacte
AL021897 Mycobacte
AL021847 Mycobacte
X17207 Chlamydomon
AL021841 Mycobacte
AB025226 Gallus ga
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M93696 Plasmid RP4
L27758 Birmingham
Ac009249 Drosophil
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AL022004 Mycobacte
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AF017113 Bacillus
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"The Pseudomonas syringse Hrp pathogenicity island has a tripartite structure composed of a cluster of type III secretion genes bounded exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants; Proc. Natl. Acad. Sci. U.S.A. 97(9):4856-4861(2000).
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J. Bacteriol. 180(19):5211-5217(1998).
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1-20052
                                                            source
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PUBMED; 10781092.
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Bacteria; P
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Q9JP34;
                                                                                                                                                                                                            Q9JP31;
Q9JP32;
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Proteobacteria;
                                                                                                                                     Q9JP37;
                                                                                                                                                   Q9JP36;
                                                                                                                                                                    Q9JP35;
                                                                                                                                                                                                                                           Q9JP30;
                                                                                                                                                                                                                                                           Q9JP29;
                                                                                                                                                                                                                                                                         Q9JP28;
                                                                                                                                                                                                                                                                                       Q9JP27;
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                                                                                                                                                                                                                                                                                                                                                                                           Collmer A.;
/note="conserved effector locus
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087264.
09JP28.
09JP28.
09JP29.
09JP31.
09JP31.
09JP33.
09JP34.
09JP34.
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09JP35.
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Last updated,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tomato; gamma
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                             flanking the
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VNLTTPFI ILADKATGLWPTAGATGNRNY LINAERCEGGVTLVLISEGAGNVSGGFGAG
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complement(8226...8621)
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LTONGIALAGGFAGVGKLQEMATKNITDBATKAAYSQLTNLAGSAAVFAGATWTTAALTTD
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NMLKASIIGNVAGIAHETVNSVVKPMFQAALQKTGLNERLNMVPMKAVDTNTVIPDFFE
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EVDGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQ
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NMALAATGSVSYLSTLYTNQSYTAEBKALKAAGMGGATPMLDRTETL"
complement(10828. .11322)
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Query Match Best Local S Matches 1727 cctctgagtgcggtgcggagcaataccagtcttcctgctggcgtgtgcacactgagtcgc CTGAGTGCGCAGATTTCGTTGATAAGGGTGTGGTACTGGTCATTGTTGGTCATTTCAAGG ctgagtgcgcagatttcgttgataagggtgtggtactggtcattgttggtcatttccaagg 1727; Similarity Conservative /product="unknown" /protein\_id="AAF71505.1" 99.88; 0; Score 1725.8; Pred. No. 0; Mismatches DВ 2; 16; Indels Length 20052; 0; Gaps 11329 120 0;

transl\_table=11

/note="ORF6"

db\_xref="SPTREMBL:Q9JP33"

codon\_start=]

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PAVKKAESFIQDTVKSTASSTTGYVADQTVKLAKTVKDMGGEAITHTGASLRNTVNNLR QRPAREADIEEGGTAASPSEIPFRPMRS"

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Deng,W.L., Preston,G., Collmer,A., Chang,C.J. and Huang,H.C.

Characterization of the hrpC and hrpRS operons of Pseudomonas syringae pathovars syringae, tomato, and glycinea and analysis of the ability of hrpF, hrpC, hrpC, hrpT, and hrpV mutants to elicit the hypersensitive response and disease in plants

J. Bacteriol. 180 (17), 4523-4531 (1998)

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J. Bacteriol. 180 (19), 5211-5217 (1998)
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Preston, G., Huang, H.C., He, S.Y. and Collmer, A.

Preston, G., Huang, H.C., He, S.Y. and Collmer, A.

The HrpZ proteins of Pseudomonas syringae pvs. sy
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Alfano, J.R.,
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Sequence update by submitter
On Mar 14, 2001 this sequence version replaced gi:3228544 gi:790906
gi:3228541 gi:8037790 gi:11276506.
Location/Qualifiers
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Direct Submission
Submitted (05-MAR-2001) Plant Pathology, Cornell University, 334
Plant Sciences Bldg., Ithaca, NY 14850, USA
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Alfano,J.R., Charkowski,A.O., Deng,W.L., Badel,J.L.,
Petnicki-Ocwieja,T., van Dijk,K. and Collmer,A.
The Pseudomonas syringae Hrp pathogenicity island has a tripartite mosaic structure composed of a cluster of type III secretion genes bounded by exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants proc. Natl. Acad. Sci. U.S.A. 97 (9), 4856-4861 (2000)
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Sequence update by submitter
8 (bases 1 to 52498)
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Ramos, A.R., Rehm, A.H.
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HHAVDAADKTKVDGNVDAEDLKGLAQSNPGLSGALKQSCSTWSQPGFLGQVDEAGMSG
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Query Match
Best Local Sim
Matches 1727;
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complement(10560.
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/protein_id="AAC62530.1"
/protein_id="AAC62530.1"
/db_xref="GI:3695001"
/translation="MSIGINSSTSYQPASTQLDFSALSGKSPQTNTFSDESTAQGVDP
SALLFDTARQKDVSFGQPDNTVQNPTDSSAATDPQSNVYKLLSALVTSLLQMLMNLNK
KQDTGQDSNEWQDPFQNEGGLGTPSABGSDGGTQEAASGGDEGGGTTAATGGDGGGGST
PTTEGDGGGTSPTAEGDGGGSYVTGADGSGRAPSTEDGTGGGGGSDGVTPQTPQLAN
PGRNSCNGTVSDTTGSLEQSGEVNVYKDTIKVGAGQVEDGHGATFTAAKSMGTGDQDE
HQKPLEELAEGAVLKNVNLGENEADGIHVNNKNSEQVTIDNVHAQNGEDM.TVKGEG
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/function="pectate binding"
/note="HrpW; harpin"
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LNGVDATHGKFALVKSDSDDLKLATGDIAMTDVKHAYDKTKASTQHTEL"
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                                           gaagaatgtgaacctgggtgagaacgaggtcgatggcatccacgtgaaagccaaaaacgc 1296
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                                                                                                GAAAAACGTGAACCTGGGCGAGAACGAAGCCGACGGCATCCACGTGAATGCCAAAAACTC
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Lorang, J.M. and Keen, N.T.
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198 c 185 g` 146 t
                                                                                                                                                                              /evidence=not_experimental
/product="unknown"
/protein_id="AAC43432.1"
/db_xref="GI:563241"
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                                                                                                                                                                                                                                                     /note="avrE locus"
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Riverside, CA 92521, USA
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Kim,J.F. and Beer,S.V.
Direct Submission
Submitted (18-MAR-1997)
                                                          Kim,J.F. and Beer,S.V.
HrpW of Erwinia amylovora, a new harpin that contains homologous to pectate lyases of a distinct class J. Bacteriol. 180 (19), 5203-5210 (1998)
                                                                                                                                I (bases 912 to 2255)

Kim, J.F., Zumoff, C.H. and Beer

HrpW, a new harpin of Erwinia

pectate lyases
                                                                                                                                                                                     Erwinia amylovora
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                         U94513 2708 bp
Erwinia amylovora disc
hrpW operon, complete
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                                                                                                        Phytopathology 87, S52 (bases 1 to 2708)
                                                                                                                                                                                                                 Erwinia amylovora.
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                                                                                                                                                                               Erwinia
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a disease-specific conplete sequence.
                                                                                                                     (1997)
  Plant Pathology, Cornell University,
                                                                                                                                                      Beer, S.V
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Location/Qualifiers
                                                                                                                                                                                        /translation="mmmksaerppaeswvdvvnsqqhlspaqyqafqkaidqvqqrhh
Qvlsrpmpqrqgkfeldsfvdsthadfligdsdrsdsnvgqtammitryladrllelq
                                                                                                                                                                 ITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVRTNGGQQ
GNWDLNLSHISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAEGKNRGKMPRIHQPSTAADGISAAHQQKKSFSLRGCLGTKKFSRSAPQGQPGTTHS
KGATLEDLLAKDDGETQHEAAAPDAAELTRSGGVKRRNNDDMAGRPMVKGGSGEDKVP
TQQKRHDLNNEGQMRQTMLSKMAHPASANAGDRLQHSPPHIPGSHHEIKEEPVGSTSK
ATTAHADRVEIAQEDDDSEF*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Hrp-secreted pathogenicity/avirulence
similar to Pseudomonas syringae AvrE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<1. .714)
/gene="dspE"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="disease-specific complement(<1...729)
                              /product="potential HrpW-specific
/protein_id="AAC62316.1"
/db_xref="GI:3414588"
                                                                                                                                                                                                                                                                                                                                                                                cysteine"
                                                                                                                                                                                                                                                                                                                                                                                        /gene="hrpW"
/function="elicit the hypersensitive reaction"
/note="Hrp-secreted; C-terminal domain similar to class
/note="Hrp-secreted; C-terminal domain similar to class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="disease-specific operon"
/note="HrpL-dependent promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(755. .784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(724. .729)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="DspE"
/protein_id="AAC62315.1"
/protein_id="AAC62315.1"
/db_xref="GI:3414587"
/translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSPQNAAASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="dspE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Ea321; ATCC /
/db_xref="taxon:552"
/db_xref="ATCC:49947"
                                                                                  /transl_table=11
                                                                                                 /codon_start=
                                                                                                                /note="putative;
                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="hrpW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="hrpW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="a strain that infects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Erwinia amylovora"
/strain="Ea321; ATCC 49947"
                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="harpin gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="hrpW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="HrpL-dependent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene=
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                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATCCCACGTTGAAATCACTAACAGTTCCTTCGAGCACGCCTCTGACAAGATCCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gccggcaagatcaatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgac 1138
                                                                                                                                                                                                                                                                                                                                                                                AGTGATATCTCACTGGGTGATGTTGAAAACCACTACAA 2218
                                                                                                                                                                                                                                                                                                                                                                                                 ggcaacatcgccatgaccgacgtcaaacacgcctacga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACGCACTAACGGCGGTCAACAG---GGTAACTGGGATCTGAATCTGAGCCATATCAGC 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttcgcaccaacggtggcaagcagtttgatgacatgagcatcgagctgaacggcatcgaa 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAATGCCGATACTAACCTGAGCGTTGACAACGTGAAGGCCAAAGACTTTTGGTACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcaacgccaacactcacttgaaaatcgacaacttcaaggccgacgatttcggcacgatg 1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAAACCGCTGTTTATACTGGAAGACGGTGCCAGCCTGAAAAACGTCACCATGGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAAAGGACAAACCTTCACCGCCGGTTCAGAATTAGGCGATGGCGGCCAGTCTGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330;
                                                                                                                                                                                                                                                                 Erwinia
Y13831
 Direct Submission
                                                                                                 DspA, an essential pathogenicity factor of Erwinia amylovora showing homology with AvrE of Pseudomonas syringae, is secre
                                                                                                                                                                                                              dspA gene; dspB gene;
Erwinia amylovora.
                    Gaudriault,S.
                                                                                the Hrp secretion pathway in a DspB-dependent way
                                                                                                                                 Gaudriault, S., Malandrin, L., Paulin, J.P.
                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                 Erwinia amylovora
                                                                                                                                                                                                                                                  Y13831.1
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                                 (bases 1 to 9985)
                                                                                                                                                (bases 1 to 9985)
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2655. .2692
/gene="hrpW
                                                                                                                                                                                                                                                  GI:3150149
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                                                                                                                                                                                                                                                                                hrpW,
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                                                                                                                                                                                                                               hrpW
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dspA,
                                                                 1057-1069 (1997)
                                                                                                                                                                                gamma subdivision;
                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                dspB,
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                                                                                                                                 Barny, M.A.
                                                                                                                                                                                   Enterobacteriaceae;
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Gaudriault,S., Brisset,M.N. and Barny,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAY-1998) S. 75231, Paris, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JUN-1997) S. Gaudriault, INRA, 16 rue Claude Bernard 75231, Paris, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Erwinia amylovora, a new Hrp-secreted
                                               /product="bypa protein"
/protein_id="CAA74156.1"
/protein_id="CAA74156.1"
/db_xref="g1:2695858"
/db_xref="g1:2695858"
/db_xref="g1:2695858"
/db_xref="g1:2695858"
/db_xref="sptrembl:054581"
/translation="melksigtehkaavhtaahnpvghgvalqogssssspqnaaslaaegkrngknprihopstaadoisaahqokksfsilgcleftkkfsrsappogpgtths
AAEGKRNGKNPRIHOPSTAADOISAAHQOKSFSILGCLGTTKKFSRSAPPOGPGTTHS
KASTLEDLLARDDGETOHEAAADOISAAHQOKLSFSHIFGSHHEIKEEPVGSTSK
KASTLEDLLARDDGETOHEAAAPDAARLTRSGGVKRNDDMAGRPWKGGSGEDKVP
TQQKRHQLNNFGQMRQTMLSKMAHPASANAGDRUGHSPHIPGSHHEIKEEPVGSTSK
ATTAHADRVEIAQEDDDSEFQQLHQORLARERNPPQPFLGVATPISARFQPKLTAV
AESVLEGTDTTOSPLKPQSMLKGSGAGVFLAVLDKGKLQLAPDNPPALNTILKQTL
GKDTOHYLAHHASSDGSQHLLLDNKGHLFDIKSTATSTSVLHNSHPGEIKGKLAQAGT
GSVSVDGKSKKISLGSGTQSHNKTMLSQPGEAHRSLLTGIWQHPAGAARPQGESIRLH
DDKIHIIHPELGVWQSADKDTHSQLSRAPGKLYALKDNRTLQKULSDNKSSEKLVDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lett. 428 (3), 224-228 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSYSVDQRGQVAILTDTPGRHKMSIMPSLDASPESHISLSLHFADAHQGLLHGKSELE
AQSVAISHGRLVVADSEGKLFSAAIPKQGDGNELKMKAMPQHALDEHFGHDHQISGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="dspA"
3076. .8662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="HrpW protein"
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.3035)
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   Conservative
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a 2562 c 2726 g 2127 t
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                                   9.0%;
57.1%;
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                               Score 155.2; DB 2
Pred. No. 2.1e-20;
Mismatches 233;
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   Indels
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GTACGCACTAACGGCGGTCAACAG---GGTAACTGGGATCTGAATCTGAGCCATATCAGC 1740

transl\_table=11/

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ACCESSION
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SOURCE
ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gctaaccacggcaagttcgccctggtgaaaagcgacagtgacgatctgaagctggcaacg 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGAAGACGGTAAGTTCTCGTTCGTTAAAAGCGATAGCGAGGGGGCTAAACGTCAATACC 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF083620 4291 bp DNA BCT 12-APR-2000 Erwinia amylovora harpin HrpN (hrpN) gene, partial cds; potential ORFB-specific chaperone, virulence/avirulence effector protein homolog, probable HrpW-specific chaperone, and harpin HrpW genes, complete cds; and Hrp-secreted pathogenicity/avirulence protein DspE (dspE) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-AUG-1998) Plant Pathology, Co
Plant Science Bldg., Ithaca, NY 14853, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 4291)
Kim, J.F., Zumoff, C.H. and Beer, S.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, J.F., Laby, R.J. and Beer, S.V. Comparison of the hrpN-flanking r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erwinia amylovora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision;
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Salmonella enterica, pseudotuberculosis "
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                 /note="ORFB; similar to ORFB of Erwinia amylovora
AvrRxv of Xanthomonas campestris pv. vesicatoria,
Salmonella enterica, and YopJ of Yersinia
                                        AvrRxv of Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="pathogenic to
<1. .429</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              'note="ORFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="HrpN family harpin"
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                                                                                                                                                                                                                                                                                         member of SycH family of chaperones and
ce proteins; leucine-rich*
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                               a Ea321,
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1079 gccggcaagatcaatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgac 1138

Query Match Best Local Similarity Matches 329; Conserv

Conservative

0;

Score 153.6; DB 1; Pred. No. 5.1e-20; 0; Mismatches 234;

Length 4291; Indels

15;

Gaps

2

56.9%;

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BASE COUNT
ORIGIN
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                             996
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                                                  AAEGKNRGEMPRI"
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SSGTSSSGGSPFNNLSGGKAPSGNSPSGSYSPVSTESPPSFTPTSPTSPLDFPSSPTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="HrpW family harpin; class III pectate lyases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNWDLNLSHISAEDGKFSFVKSDSEGLKVNTSDISLSDVENHYKVPMSANLKVAE"
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QLEQQRG"
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RIQNSEWDCIMYSLNNALKSFKHHDEYTARLHKGEKIPVPAEFFKHAQSKSMVEGLPH
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                                                                                                                                                                                                                                                          1120. .>4291
/gene="dspE"
/note="similar to
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/note="HrpL-dependent promoter
1105. .>4291
/gene="dspE"
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/protein_id="AAF63401.1"
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                                                                             translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSSPQNAAASL
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185. .192
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=mBK20
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://cCR-081.mit.edu/GENSCAN.html),
MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
                                                                                                                                                                                              Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                     Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned P1 and TAC clones DNA Res. 5 (1), 41-54 (1998)
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356. .363
/note="Chi
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/note="Chi
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Pred. No. 0.0033;
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CDS

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.lastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denmark, http://www.cbs.dtu.dk/services/NetGene2/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAVLNFPLDAGKYEAPANSGRKRKRSDVHEELQRTQSNSSSSSCDAF" complement(j0in(2200. .2567,2679. .2786,2884. .2'3043. .3219,3367. .3855,4103. .4219)) /note="gene_id:MBK20.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(5140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCLDKISYIEWALDSEYILCGLYKKPMIQAWSLTQPEWTCKIDEGPAGISYARWSPDS
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LLSCQSWEIMGSFAVDTLDLADLEWSPDDSSIVVWDSPLEYKAYECGLGVKTVSWSPC
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FPEMIRTEYYTDRRIYAFSVIGFVKEETDAASYILLHIPNQAVKYNFIDKTFKKLCDF
                                                                                                                                                                                                                                                                                                                                                     similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                          gene_id:MBK20.4
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note="emb|CAB85517.1
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/strain="Columbia"
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EKKKAMKQIDLRRANDTEIMLTKVNIPLADMMAAVLGMDEYYLDVDQIENLIRECPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(16863...16984,17088...17154,17272...1734(17462...17578,17642...17713,17790...17884.18056...18137,18232...18282,18422...18574,18643...18684,18782...18880,18966...19037,19148...19216,19525...19593,19716...19832,19908...19979,20055...20122,20745...20826,20904...20954,21053...21133,21251...21292,21434...21532,21630...21734,21845...21917,22031...22302))
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gene_id:MBK20.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to unknown protein"
/codon_start=1
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CCSPSPSLRPNVKQVLRKLEEIGKF"
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/note="contains similarity to receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/protein_id="BAB11443.1"
/db_xref="GI:9759586"
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pir||T17454
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13356. .13447,13592. .13601,13826. .13897,14025. .14162,
14266. .14421,14707. .14845,14945. .15011)
/note="gb|AAD38624.1
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/protein_id="BAB11440.1"
/db_xref="GI:9759583"
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/product="tRNA-Leu(CAA)"
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Best Local S
Matches 112
                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                            JOURNAL MEDLINE
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                                                                JOURNAL
                                                                                                                                                                                                             REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggcggtggcggcggtgatactccgaccgcaacaggcggtggcggcggcagcggtggcggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcggggggcggcggtacaccggatgcgacaggtggcggcggcggtgatacgccaagcgcaa 860
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                                                                                                                                                                                                                                                                                                                  Cole's.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III.C.E.,
Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quall,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S: and
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
   Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcor Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv complete AL022022 AL123456 AL022022.1 GI:3261554
                                                                                                                       Parkhill, J
                                                                                                                                                                                                                                                                    complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 47852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                            Direct Submission
                                                                                                                                                                                                          Erratum: [[published erratum appears in Nature 1998 Nov
                                                                                                                                                   12;396(6707):190]]
2 (bases 1 to 47852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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LKSLAEEIQAITKGLEKLNKQLTASESDGPVSQVFRKVLKDFISMAETQVATVSSLYS
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/product="SMC-like protein"
/protein_id="BAB11444.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47852 bp
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Pred. No. 0.0026;
0; Mismatches 77;
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                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                  RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:2924430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiation codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         renumbered from the original cosmid submissions but the odesignations are in brackets after the new gene numbers prediction was based on a Hidden Markov Model of TB genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv3494c, (MTV023.01c), len: 564. Unknown Pro-rich protein similar to several Mycobacterium tuberculosis proteins e.g. MTCI28.14 (515 aa), MTCI9H5.28c (516 aa) and (MTV051.09). Has hydrophobic stretch, possibly signal peptide at N-terminus. FASTA scores: 297050/MTCI28_14 (515 aa) opt: 1006 z-score: 582.8 E(): 5.9e-25; 34.3% identity in 559 aa overlap; 297182/MTCY19H5.28 (516 aa) opt: 979 z-score:567.7 E(): 4.1e-24; 33.5% identity in 555 aa overlap. TBparse score is 0.897"
/note="Rv3495c, (MTV023.02c), len: 384. lprN, similar Mycobacterium tuberculosis proteins MTC128.13 (390 aa) MTC119H5.29 (402 aa) and (MTV051.08). Probably lipoprotein, contains possible signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site. FASTA scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xtef="sptrembl:053539"
/translation="midrlakiqusifavitvitlsvmaifylklpatfgigtygvsa
/translation="midrlakiqusifavitvitlsvmaifylklpatfgigtyrsvs
Dfvaggglyknanvtyrgvavgrvesvglnpmgvtahhrlusgtaifsvrsvs
Algeqyidlvppenps3tklrmgfrigmgntrigqdvadllrqaffillgslgdtrlre
Liheafiatmgafpelarliesarllvdeananypqvsglidqafffilgagdi
Ksladglarftwqlraadpralfaltabapdaifargirpegfrysglippegfrysglipper
Vgviyhksieglivpfpalfalitsaggvpqbegakldfkidlhdpppcmtgfilpp
Lvrspadesvetipromycktaqudesvrgarnypqqeffekaptvqlcrdprgyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:1773"
/clone="Y13E12"
<1. .47852
                                                                                                                                                                                                                                         complement(1706.
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                                                                                                                                                                                                                                                                                                                            PAPHOPAOPAPPPNDNGPPPFTSWMPPGYPPEPPQVPYPATIPPPPPPEGTGPPPGPAPGPQPQASGPAYTIYDOLSGAFADPAGGTGIFAPGMTGASSAENWVDLMRDPRQL"
complement(1703...1707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv3494c"
/note="pv7240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv3494c"
complement/
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physical clone"
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/strain="H37Rv"
                                                                                                                                                                                                                   complement(1706. .2860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein Rv3494c"
/protein_id="CAA17731.1"
/db_xref="GI:2924431"
                                                                                                                                                                                                                                                                       /note="possible RBS for
complement(1706. .2860)
                                                                                                                                                                                                                                                                                                                                                                                                                              PVGTNPWRGPPIPYGTEVTDGRNILPPNKFPYIPPGADPDPGVPIVGPPPPGQVAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:1773"
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/note="Rv3496c, (MTV023.03c), len: 451. Unknown but similar to Mycobacterium tuberculosis proteins MTC128.12 (530 aa), MTCY19H5.30c (508 aa) (MTV051.07). Hydrophobic region at N-terminus. FASTA scores: Z97050)MTC128.12 (530 aa) opt:838 z-score: 711.0 E(): 4.3e-32; 35.1% identity in 473 aaoverlap; and Z97182]MTC19H5_30 (508 aa) opt: 821 z-score:697.0 E(): 2.6e-31; 35.1% identity in 453 aa overlap. TBparse score is 0.891"
                                                                                                                                                                                                                                 note="Rv3497c, (MTV023.04c), len: 357. Unknown but Similar Mycobacterium tuberculosis proteins MTCY19H5.31 (481 aa), MTC128.11, (515 aa)and MTV051.06. Hydrophobic region atN-terminus. FASTA scores: Z97182|MTCY19H5_31 (481 aa) opt:611 z-score: 667.7 E(): 1.1e-29; 32.5% identity in 332aa overlap; and Z97050|MTC128_11 (515 aa) opt: 587 z-score:641.2 E(): 3.3e-28; 30.1% identity in 3335 aa overlap. TBparse score is 0.889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2857. .4212)
/gene="Rv3496c"
complement(2857. .4212)
/gene="Rv3496c"
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/gene="Rv3496c"
/note="possible RBS for
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4209. .5282)
/gene="Rv3497c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPLGAAINQAADTLDGNGDSLHNALRELAQVAGRLGDSRGDIFGTVKNLQVLVDALSE
SDEQIVQFAGHVASVSQVLADSSANLDQTLGTLNQALSDIRGFLRENNSTLIETVNQL
NDFAQTLSDQSENIEQVLHVAGPGITNFYNIYDPAQGTLNGLLSIPNFANPVQFICGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFTSAVGLYPGDQVRVLGVPVGEIDMIEPRSSDVKITMSVSKDVKVPVDVQAVIMSPN
LVAARFIQLTPVYTGGAVLPDNGRIDLDRTAVPVEWDEVKEGLIRLAADLSPAAGELQ
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TFFTTAYFDPNMAHMDEILNPPDFLIGELANLSGQAADPFKIPPGTASGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNRIWLRAIILTASSALLAGCQFGGLNSLPLPGTAGHGEGAYSV
TVEMADVATLEQNSPVMVDDVTVGSVAGTVAVQRDEGSFYAAVKLDLDKNVLLPANAV
AKVSQTSLLGSLHVELAPPTDRPPTGRLVDGSRITEANTDRFPTTEEVFSALGVVVN
AKVSQTSLLGSLHVELAPPTDRPPTGRLVDGSRITEANTORFPTTEEVFSALGVVNV
KUVGALEEIIDETHQAVAGRQAQFVNLVPRLAELTAGLNRQVHDIIDALDGLNRYSAI
GNVGALEEIIDETHQAVAGRQAQFVNLVPRLAELTAGLNRQVHDIIDALDGLNRYSAI
LARDXDNLGRALDTLPDAYRVLNQNRDHIVDAFAALKRLTMVTSHVLAETKVDFGEDL
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0; 33.6% identity in 363 aa overlap; and
Z97182|MTCY19H5_29 (402 aa) opt: 572 z-score: 667.9 E
1.1e-29; 31_8% identity in 362 aa overlap. TBparse
/translation="mlnrkpsskherdplrtgffglvlvfcvvlfafgysglpfwpQg
KTYDAYFTDAGGITPGNSVYVSGLKVGAVSAVSLAGNSAKVTFSVDRSIVVGDQSLAA
IRTDTILGERSIAVSPAGSGKSTTIPLSRTTPYTLNGVLQDLGRNANDLNRPQFEQA
                                                                                                   /product="hypothetical protein Rv3497c"
/protein_id="CAA17734.1"
/db_xref="GI:2924434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATEAKSETPVPELTWVPAGGGAPVGNPADLQSLLVPPAPGPAPAPPAPGAGPGEHGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein
/protein_id="CAA17733.1"
/db_xref="GI:2924433"
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/product="lprN"
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/translation="MMGRVAMLTGSRGLRYATVIALVAALVGGVYVLSSTGNKRTIVG
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/db_xref="GI:2924432"
                                                                                  /db_xref="SPTREMBL:053542"
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Query Match
Best Local Similarity
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Streptomyces
                                                        histidine kinase; two component system response uracil DNA glycosylase.
                                                                                                                ABC transporter ATP-binding protein; ABC transporter transmembrane protein; asnC-family transcriptional regulatory protein; hydrolase; integral membrane protein; lipoprotein; mark-family transcriptional regulator; oxidoreductase; oxidoreductase, iron-sulphur binding subunit; oxidoreductase, molybdopterin binding subunit; regulatory protein; secreted deacetylase; secreted lyase; secreted protein; teR-family transcriptional regulator; two component system
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Streptomyces
                             Streptomyces
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KLVEDGNQLFAALDARRAALSALISGIDDVAAQISGFVADNRKEFGPALSKLNLVLAN
LNERRDYITEALKRLPTYATTLGEVVGSGPGFNVNVYSVLPGPLVATVFDLVFQPGKL
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/protein_id="CAA17735.1"
/db_xref="GI:2924435"
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                             coelicolor.
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Pred. No. 0.0054;
D; Mismatches 211
                                                                                                                                                                                                                                                                                                                                                                                                                   cosmid 2G38
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                            regulator; ung,
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JOURNAL REFERENCE
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The more
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Submitted (13-OCT-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, (3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pb before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The lengti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overlap between neighbouring submissions. Cosmid 2G38
                                                                                                                            /Clone="cosmid 2G38"
complement(1. .320)
/gene="2SCG38.01c"
complement(21. .320)
/gene="2SCG38.01c"
/note="2SCG38.01c, possible regulatory protein(fragment),
/note="2SCG38.01c, possible regulatory protein(fragment),
len: >106 aa; similar to N-terminal region of TR:CACO1635
(EMBL.AL391072) Streptomyces coelicolor putative
regulatory protein SC9A4.08, 116 aa; fasta scores: opt:
218 z-score: 308.8 E(): 9.3e-10; 46.28 identity in 91 aa
/product="putative regulatory protein(fragment)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Streptomyces coelicolor A3(2)"
/strain="N3/2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Streptomyces
/db_xref="taxon:1902"
                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor'
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/gene="2SCG38.03"
1739. .2530
                                                                                                                                                                                                                                                                                                                                  complement(2544. 3350)

/gene="25CG38.04c"
/note="25CG38.04c, conserved hypothetical protein, len:
/note="25CG38.04c, conserved hypothetical protein, len:
268 aa; similar to TR:053782 (EMBL:AL021943) Mycobacter;
tuberculosis hypothetical 26.5 kDa protein MTV040.02, 24
aa; fasta scores: opt: 735 z-score: 848.5 E(): 0; 51.48
identity in 218 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative secreted lyase"
/protein_id="CACl3062.1"
/protein_id="CACl3062.1"
/db_xref="G1:10803134"
/translation="MTAVTRPRARRAVTGALGALGLSVGMLMTSGASSAQAATWPTPN
/translation="MTAVTRPRARRAVTGALGALGLSVGMLMTSGASSAQAATWPTPN
GSEGVSSTLSVSGTKDYGMKRLYGTGDLGSGGGDEDGCFILELAFGAVLKFQTFQAFA
ADGVHCKGSCTLQNVWMEDVGEDAATTRGSSSAVYTVSGGAKAEADDKVKFQTGAGAFA
LNISGFAVKNFGTFVRSCGNCSTQYRRTINLNGIEVNWKGGRIAGINTNYGDSATLRN
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/note="2SCG38.03, probable secreted lyase, len: 266 aa;
/note="2SCG38.03, probable secreted lyase, len: 266 aa;
similar to TR:004701 (EMBL:M94691) Fusarium solani pectate
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
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lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
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lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
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lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
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lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.2) PelA, 242 aa; fasta scores:
lyase A precursor (EC 4.2.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Pfam match to entry PF00724 oxidored_FMN, NADH:flavin oxidoreductase / NADH oxidase family 318.10, E-value le-91"
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DAVREVWPDDKPLFFRVSATDWLEEGGWTPDDTVRFARDLEAHGIDLLDVSTGGNVPR
VRIPTGPGYQVPFAARVKAGSTLPVAAVGLITEPGQAEKILANGEADAVLLGRELLRN
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/protein_id="CAC13061.1"
/db_xref="G1:10803133"
/db_xref="G1:10803133"
/tabslation="MGALFEPFRLRDTIPNRIWMPPMCQYSAAPEGPSAGVPGDWHF
AHYGARAVGGTGLIVVEATGVSPEGRISPQDLGLWNDTQVEAFRRITGFLRSQGTVPA
VQLAHAGRKASTAQPWRGGAPVGADAYGWQPLAPSALAFDERHEYPTELTVPQIQEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="2SCG38.04c"
complement/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide sequence"
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/db_xref="GI:10803132"
/tanslation="MyPBATAAGTRELPHPTRAEIRLEGVLHALSDPVRLRIVRDLAA
/translation="MyPBATAAGTRELPHPTRAEIRLEGVLHALSDPVRLRIVRDLAD
DSGALFSCSHFDLPVTKSTTTYHFRVLRESGVIRQTYRGTAKMNGLRRDDLDIVFPGL
                                                           /protein_id="CAC13063.
/db_xref="GI:10803135"
                                                                                                                                                                       /product="conserved hypothetical
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162. .1541
translation="MGARTVRAHVDERRGAARMTGSGDPGRLTLRPLSARSVILSLLL/
                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                              /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITIVGDSSKKIVPCQKYIGNDDGDEPDSNGSGADGTYCKYSSSDITYK"
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                                                                                                                                                                 protein"
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Query Match
Best Local Similarity
Matches 211; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                     cgttgaagaatgtgaacctgggtgagaacgaggtcgatggcatccacgtgaaagccaaaa 1292
tg---agcatcgagctgaacggcatcgaagctaac 1564
                                                          TCGCCGTCAAGAACTTCGGCACCTTCGTCCGGTCCTGCGGCAACTGCTCGACGCAGTACA
                                                                                               tcaaggccgacgatttcggcacgatggttcgcaccaacggtggcaagcagtttgatgaca 1532
                                                                                                                                                                                CCTTCCGGGGCTCGTCGTCGAACGTC-----TACACCGTCTCCGGCGGCGCCGCCA
                                                                                                                                                                                                                                                                 cggtcaaaggcgagggaggcgcagcggtcactaatctgaacatcaagaacagcagtgcca 1412
                                                                                                                                                                                                                                                                                                                 GCACGC-----
                                                                                                                                                                                                                                                                                                                                                   acgctcaggaagtcaccattgacaacgtgcatgcccagaacgtcggtgaagacctgatta 1352
                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGAAGAACGTGATCATCGGCGCCCCCGGCCGCGGACGGCGTGCACTGCAAGGGCAGTT 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCTCCGGCGGCCAGGACGAGGACCAGGGCCCGATCCTGGAACTGGCTCCCGGCGCCC 2012
                                                                                                                                           AGGAGGCCGACGACAAGGTGTTCCAGTTCAACGGCGCCGGAACGCTGAACATCTCCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="25CG38.05, probable oxidoreductase, len: 567 aa similar to SW:AIDB_ECOLI (EMBL:L20915) Escherichia col oxidoreductase AldB protein, 541 aa; fasta scores: pt 1437 z-score: 1553.6 E(): 0, 45-8% identity in 517 aa overlap. Contains 2x Pfam matches to entry PF00441 Acyl-CoA_dh, Acyl-CoA dehydrogenase and match to Prosientry PS00073 Acyl-CoA dehydrogenases signature 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to dehydrogenase, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAVPALRAQPELAEVYEPLLTSREYEPGLRTPTDKRGLLAGMGMTEKQGGSDVRTNAT
ATATAEPGYYTLROHKWFTSAPMCDVFLVLAQAAGGLSCFLVRVLPDGTRRYTFRVQ
RLKDKLGNRSNASSEPEFDGTVAMLVGPEGGVKTI IEMVCTRLDCVMASATLMKRT
LVEAGHHVRHRTAFGARLVDQPLMRNVLADLALESEAATALTLRLAGAADRAVRGDEG
EAAFRRIATAYGKYWYTKRGPAFTAEALECLGGNGYVESSGMPHHYREAPLLSINEGS
GNVNALDVLRALGRSPAAAQALFGELSLARGADARLDAAADRLRTGLTEASETGARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTTLAQEPPYESYEPSEEPWGRPEGYATHDVTNQPPPLAPYDAS
DDTVLLEGLRREGAGWAEDGLRRLGRRAGSAQAQDWGDLANRHEPVLRTHDRYGNRVD
EVEYHPSWHHLMRVAVGEGLAGAPWADGRPGAHVARTAGGLVWGHTEAGHGCPTSMTY
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QDEALRPHTRAMDGDWETLVITATGRDPAARAELRTRLAALRLAELREGVWLRPANLD
RPLPTDLGRVAERLVSRPGSPAVELAARLWPLVDWADTARALLVHVDRARRPAGLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to dehydrogenase, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative oxidoreductase"
/protein_id="CAC13064.1"
/db_xref="gI:10803136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAAVVRHLLADPVLPPELLPPDWPGTALRDAYARYQREQSGQVRAHGPRT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.6%;
                                                                                                                                                                                                                                                                                                              -TCCAGAACGTCTGGTGGGAGGACGTCGGCGAGGACGCGGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 0.015;
0; Mismatches 163;
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2.10, E-value 8.7"
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AUTHORS
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AF017113/c
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TITLE
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SOURCE
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98230327
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             /gene="yvjA"
1350. .2195
/gene="yvjA"
                                                                              /gene="yvjA"
1338. .2195
                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="prfB"
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Robinson,C., Rivolta,C., Karamata,D. and Moir,A. The product of the yvoC (gerF) gene of Bacillus required for spore germination Microbiology 144 (Pt 11), 3105-3109 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lazarevic, V., Soldo, B., Rivolta, C., Reynolds, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiol. 27 (6), 1157-1169 (1998)
/note="similar to thermophilic bacterium protein: PIR Accession Number S43727 and subtilis yqfU, YpjC and YitB proteins" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVETLDYLPGDEAGIKSVTLLIKGHNAYGYLKAEKGVHRLVRISPFDSSGRRHTSFVS
CEVMPEFNDEIDIDIRTEDIKVDTYRASGAGGQHVNTTDSAVRITHLPTNVVVTCQTE
RSQIKNRERAMKMLKAKLYQRRIEEQQAELDEIRGEQKEIGWGSQIRSYVFHPYSMVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative peptide chain release factor RF-2"
/protein_id="AAC67303.1"
/db_xref="GI:2618874"
/tdb_xref="GI:2618874"
/translation="WELSEIRAELENWASRLADFRGSLDLESKEARIAELDEQWADPE
FWNDQOKAQTVINEANGLKDYVNSYKKLNESHEELQMTHDLLKEEPDTDLQLELEKEL
KSLTKEFNEFELQLLLSEPYDKNNAILELHPGAGGTESQDWGSMLLRWYTRWGERRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHRTNTEMGNVQAVMDGDIDTFIDAYLRSKLS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis"
/db_xref="taxon:1423"
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                                                                                PS-3 hypothetical to Bacillus
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                                                                      /gene="yvjb"
4525. 5967
/gene="yvjb"
/codon_start=1
/transl_table=11
/product="putative protease"
/protein_id="AAC67263.1"
/db_xref="GI:2618834"
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/codon_start=1
/transl_table=11
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/protein_id="ARG67264.1"
/db_xref="G1:2618835"
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2244. .250
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3476. .3484
/gene="ftsx"
3495. .4385
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/gene="ftsE"
2816. .3502
/gene="ftsE"
/codon_start=1
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2806. .3502
                                                                                                                                                                                                                                                                                                                                                                                     /translation="MIKILGRHLRESFKSLGRNTWHTFASISAVTVTLILVGVFLVIM
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LNLNNAATNAERQVEIKVLIDLTADQRAQDKLQNDIKELKGIGSVTFSSKEKELDQIV
DSFGDOSGKSLTMKDQSHPLNDAFVKKTTDFHDTFNVAKKIEKHDHVKKVTJGKEEVSK
LFKVVGVSRNIGIALIIGLVFTAMFLISNTIKITIFARRKEIELMKLVQATNWFIRWP
FFLEGLLLGVFGSVIFIALVLSTYQYVIGWVVPKVQGSFVSLLPYNPFVFQVSLVLIA
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/product="cell division atp-binding protein"
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4511. .5967
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FSDSLDSSFEGIGAEVGMEDGKIIIVSPFKKSPAEKAGLKPNDEIISINGESMAGKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mdvrnktlwilkdyvyiligaaitavsfnvfllpnkiaaggvsg
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IVVTAMIVFNIEQGLYAMLGYYVSSKTIDVVQVGFNISKMALIITKQEQAVKEAVLQK
                                                                                                                                                                                                                                                                                                                                                                   [GAVIGVWGSLTSIRKFLRV"
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/db_xref="GI:2618832"
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2223. .2582
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/gene="cccB"
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TTTTCGTGTGGAGGATGGAGCAACCCTGAAAAATGTGGTGCTTGGTGCACCTGCAGCTGA 37455
                                                                     gttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcga 1269
                                                                                                                                                                                               aaccttcactgccgacaaatctatgggtaacggagaccagggcgaaaatcagaagcccat 1209
                                                                                                                                                                                                                                                                                                                CAAAGTGGTGCACGAAACAATTATCGTACCAAAAAATACAACATATGACGGGAAAGGACA 37575
                                                                                                                                                                                                                                                                                                                                                             caatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgc 1149
||| |||||| |  || || || || ||
                                                                                                                                                          GCGGTTTGTGGCAGGGAAAGAATTAGGTGACGGAAGCCAGTCAGAAAACCAAGACCCTGT
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/transl_table=11
/product="YvkB"
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regulators"
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/gene="yvkA"
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ANLLFLLLSSSHSVLFLMLSLILGGLASGVGLTSMQVSSLATVDPGMSGVASGIFSTF
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//db_xref="01:261883
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6773..6
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/gene="yvkA"
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IAERNGDKKRYFSTLTHKKAYPVNVITDKGSASASEILAGALKEAGHYDVVGDTSFGK
GTVQQAVPMGDGSNIKLTLYKWLTPNGNWIHKKGIEPTIAIKQPDYFSAGPLQLKEPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYFGSIISSALIGLISGYHTLFMILFAVSIIGVFVSLGIKSDETARIEKNSA"
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6784. .7977
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6773. .7977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="YvjD"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                      Foulger, D. Fritz, C. Fujita, M. Fujita, Y. Fuma, S., Galizzi, A., Galleron, N., Ghim, S. Y., Glaser, P., Gofeau, A., Golightly, E. J., Grandi, G., Guiseppi, G., Guy, B. J., Haga, K., Haiech, J., Harwood, C. R., Grandi, G., Guiseppi, G., Guy, B. J., Haga, K., Haiech, J., Harwood, C. R., Grandi, G., Guiseppi, G., Guy, B. J., Haga, K., Haiech, J., Harwood, C. R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M. F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Kilein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Kilein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R. P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S. H., Parro, V., Pohl, T. M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S., H., Parro, V., Pohl, T. M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S., Rieger, M., Portetelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Schowska, A., Seror, S. J., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S. J., Serror, P., Shin, B. S., Soldo, B., Sorokin, A., Tamakoshi, A., Tanaka, T., Terpstra, P., Takemaru, K., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vasarotti, A., Vanier, F., Vasarotti, A., Voshikawa, H. F., Zunstein, E., Yoshikawa, H. F., Zunstein, E., Yoshikawa, H. F., Sunstein, E., K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cggtgg 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGATCGACGGCGGTTCTGCTCAAAAAGCGTCAGATAAGATATTCCAAATCAATAAAGC 37302
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Runst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bronillet, S., Brouillet, S., Broschi, C.V., Caldwell, B., Capuano, V., Cander, M.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E., Entland, R.D., Errington, J., Fabret, C., Ferrari, E., P., Paristan, M., P., Paristan, P., P
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
                                                                         Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.
                                                                                                                                                                                                                        Nature 390 (6657),
                                                                                                                                                                                                                                                              Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                           Yoshida, K., Yoshikawa, H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes;
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                                                                                                                                                      (bases 1 to 209510)
                                                                                                                                                                                                                                                                                                 complete genome sequence of the
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                                                                                                                                                                                                                                                                                                                                                                           Zumstein, E.,
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                                                                                                                                                                                                                                                                                                 gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                           Yoshikawa, H. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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                                          /protein_id="CAB15323.1"
/db_xref="GI:2635831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/protein_id="CAB15322.1"
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/strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                      /codon_start=1
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/db_xref="GI:2635829"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="yvrA"
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/protein_id="CAB15320.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yvqK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yvqK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1423"
'db_xref="SPTREMBL:034805"
                                                                                                                                                                                             note="similar"
                                                                                                                                                                                                                                                              "gene="yvrC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="GI:2635830"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="yvrB"
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                                                                                                                                                                                                                            function="unknown"
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FLLGTILLIINGRELNVMTYGEDKAKLLGVSVQQRKMMILIAGSLLTGSAVAVSGTIG
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GAPVFALILIRQHRGGRSL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SMSVSTLILTGVITNSFLGAFISLIIALTGDNLLPIVHWLLGSVSMRGWSYVILFLPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDILLQTEIPLRTLSSTPIGAGFSWSRTLIHKRLPDQPDPIEGLTACLSESGFQLQET
CAMASSERLDRFYYRTYEDGELSVFICVQTGFSIWILINGYAADQFFIKALMAAEAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to iron permease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MKLYTKTGDKGOTGLVGGRTDKDSLRVESYGTIDELNSFIGLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to iron transport system"
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FGLPIFHTIRWLVNLSKGKLEEPRNREGRPVSKNKKGKIKQPYRFFGEIFESMDQLTE
TLRRDKRNREKIQATREEWIAGLSHDLKTPLSSIYGYSMMLESKQYDWSPEEGEEMGQ
VVREKSEYMSKLIEDLNLTYRLKNDALPIERKLTSLIPFFKNVIEDFKKNPFSEGYDI
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DTPTQEIVRYSYDPQSGDVSNPEPVYENFDQSDGLPDGMTIDQNGMLWVALEGGSRVVH
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GEAGGAEKKADQLVKSMKSDLKDIQEKAKTISKDEEKSVFIEVSPDPDIYTTGKDTFM
NEMLNVIHAKNAAADQTGWVQMTDEAIVKLNPDAIVTTDGVKAKAVEKRDGWSEINAV
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LISLSRGMAEMTKGTNVTVNSVLPGPTWTEGVASYMEGAAQAAGQDTDTFIKDYFKVN
EPTSLIQRYATAEEVANTIVFLASDAASAINGTAQRVEGGIIRSL"
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KGMDEETITHLFNRYYRGTNIKDSTAGTGLGLAIAKELVHLHNGTIHVNSRTNIGTVI
                                                                                                                                                                                                                                                                                                                                                                KSSTIDYIKRKKGAIYLLDSNGKILDSINSTKSERKTMNQLELLKYSSKPWNYKREIS
VKILNKDRWMYATVPNPYYVTDQEFNKSFLKVVLKAMFLYMAVLFMYIIAMTVWYMFR
                                                                                                                                                                                                                                                                                                                                                                                                                DTLEAYLDVNEDGTWEVDNFLKKSVDKQHGWMQIIDSEGNTDYSYGVPKDVPGTYTKK
ELLSIYKTKKLHNYKLNYWAINIEDKSYLLLSGWKSKSEQLLTSVEKREQKIDSLAHY
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/gene="yvrG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLETGGYQPVPFAGDV"
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                                                                                                                                            complement(7861. .8970)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB15326.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                              function="unknown"
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                                                                       to two-component response regulator
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                                                                                                                                                                                            .8970)
                                                                       [YvrG]"
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KEYWORDS
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DEFINITION
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Best Local Similarity
Matches 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGATCGACGGCGGTTCTGCTCAAAAAGCGTCAGATAAGATATTCCAAATCAATAAAGC 190531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTCGTGTGGAGGATGGAGCAACCCTGAAAAATGTGGTGCTTGGTGCACCTGCAGCTGA
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                                                                                                                           (C12N15/0
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E32986
                                                            FR
                                                                                                                                            PI KOICHI MIZUNO, TOMOHIKO KATO, SHIGERU SATO, DAISUKE SHIBATA C12N15/09, A01H5/00, C07K16/40, C12N5/10, C12N9/10, C12P21/02// PC (C12N15/09, C12R1:91), (C12N5/10, C12R1:91), (C12P21/02, C12R1:91),
                                                                                                                                                                                                                                                                                                                                   Gene encoding cellulose synthesizer Patent: JP 2000060568-A 1 29-FEB-2000; KOICHI MIZUNO,MITSUI GTYOUSAI SHOKUBUTSU
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Koichi, M.T.K.K. and Sato, D.S.
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Search completed: October 4, 2001, 22:26:29 Job time: 7060 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

AAX24347 CDS WPI; 1999-167125/14. P-PSDB; AAW97851. Alfano JR, Charkowski A, Collmer A; 06-AUG-1997; 07-JUN-1999 (first entry) AAX24347 standard; DNA; 1729 24-JUL-1998; 18-FEB-1999. WO9907207-A1 Pseudomonas syringae pv. tomato. Hypersensitive response elicitor; dspE gene; HrpW; transgenic plant; disease resistance; insect resistance; Hypersensitive response elicitor HrpW dspE gene. AAX24347; (CORR ) CORNELL RES FOUND INC 97US-0055107. 98WO-US15501. Location/Qualifiers /\*tag= BP.

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This the DNA sequence of the dspE gene of Pseudomonas syringae pv. tomato DC3000 that codes for a 42.9 kDa hypersensitive response celicitor (HRE) polypeptide (see AAW97851), termed HrpW. To identify any HRE-like genes in the P. syringae pv. tomato DS300 DNA flanking hrpR, cosmid pCPP2357, which contains this region in vector pCPP47, was isolated. A series of subclones in pML123 were constructed and corrected for 2 potential HR phenotypes: (1) the ability to promote tobacco HRE activity in Pseudomonas fluorescens cells carrying pCPP2774, a delhrp2 pHTT11 derivative, and (ii) interference with the content of P. fluorescens cells carrying wild-type pHIR11. CC pCPP2774, a delhrp2 pHTT11 derivative, and (ii) interference with the content of P. fluorescens cells carrying wild-type pHIR11. CC second. Transcriptional unit v of this subclone contained the created DNA molecule can be used to impart disease resistance to plants. This is achieved by applying the HRE protein in a con-infectious form to plants or plant seeds. Alternatively, cc transgenic plants or plant seeds transformed with DNA encoding the CC HRE can be provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hypersensitive response eliciting (dspE) gene and protein useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
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Sequence 1729 BP; 464 A; 484 C; 486 G; 295 T; 0 other;

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Que Bes Mat	ry Ma t Loc ches	Query Match 100.0%; Score 1729; DB 20; Length 1729; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1729; Conservative 0; Mismatches 0; Indels 0; Gaps	
Qy	1	tccacttcgctgattttgaaattggcagattcatagaaacgttcaggtgtggaaatcagg 60	
ф	1	tccacttcgctgattttgaaattggcagattcatagaaacgttcaggtgtggaaatcagg 60	
Qγ	61	ctgagtgcgcagatttcgttgataagggtgtgggtactggtcattgttggtcatttcaagg 120	J
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Qγ.	301	agcaagctcaaccccaaacatccacatccctatcgaacggacagcgatacggccacttgc 360	_
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Db	361	totggtaaaccotggagotggotoggtocaattgcocaottagogaggtaacgcagcat 420	٥
Qy	421	gagcatcggcatcacaccccggccgccaacagaccaccacgccactcgatttttcggcgct 480	٥
Db	421	gagcatcggcatcacaccccggccgcaacagaccacgccactcgattttcggcgct 480	_
Qy	481	aagoggcaagagteeteaaceaaacacgtteggogageagaacacteageaagegatega 540	_
В	481	aagoggcaagagtcotcaaccaaacacgttcggcgagcagaacactcagcaagcgatcga 540	•
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                                                                                                                                                                                                                                                                                                                                                                                            is produced as part of an active defense by plants against incompatible pathogen infections. The hypersensitive response is rapid localised necrosis. The hrp protein and gene when used in nucleotide constructs are useful for providing disease resistance plants, insect control to plants, and enhancing plant growth (enhancing fruit size and earlier colouration and maturation), by direct application of the protein to plants, or by producing transgenic plants or seeds using the hrp gene.
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                                                                                                                                  The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a DNA encoding hypersensitive
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                                                                                              response elicitor protein from Erwinia amylovora. The protein is heat stable, protease sensitive and suppressed by inhibitors of plant metabolism. The present sequence is used to transform transgenic plant
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                                                            Sequence 1344 BP;
                                                                                                                                                                                    Disclosure; Page 10; 84pp; English.
                                                                                                                                                                                                           Application of a hypersensitive response elicitor protein to impart stress resistance -
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          9.0%;
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                                                                                     stress resistance.
                                                            372 C;
Score 155.2; DB 2
Pred. No. 8.3e-30;
0; Mismatches 233
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                                   05-OCT-1998;
                                                                                                                                                                                                      Erwinia
                                                                                                                                                                                                                               ornamental plant;
                                                                                                                                                                                                                                          Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; c
                                                                                                                                                                                                                                                                               DNA encoding a hypersensitive response elicitor protein
                                                                                                                                                                                                                                                                                                        08-AUG-2000
                                                                                                                                                                                                                                                                                                                                 AAA14939;
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           BIOSCIENCE CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 11-12; 100pp; English.
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hes 330;
agtgatatctcactgggtgatgttgaaaaccactacaa 1307
                        ggcaacatcgccatgaccgacgtcaaacacgcctacga 1656
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57.1%;
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Pred. No. 8.3e-30;
0; Mismatches 233;
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Best Local Similarity
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                                                                                                                                                                  1154
                                                                                                                                                                                                                                                    1094 gtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgacggccacggcgcaacc 1153
                               | 1211 ttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggttgagaacgaggtcgat 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Bacillus pectic acid lyase - useful as a food-processing agent and a fibre-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-523159/45
P-PSDB; AAW77412.
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09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, and can be produced on a mass scale.
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tttcgtctggaggctggggcaagcctgaaaaatgtagtgattggcgctcctgccgctgac
                                                                                                           tatgtggctaatccgaatacattgggggacggatcgcaggcggagaatcagaagccgatc
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 160 A; 137 C; 176 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSM-P15; pectic acid lyase; pectinic acid lyase; pectin; bod-processing; fibre-processing agent; cell wall; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pectic acid lyase encoding
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97JP-0091142.
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51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no stop codon
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                                                                                                                                                                                                                                                                                                                                  Score 58.2; DB 19;
Pred. No. 2.3e-05;
0; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koike K,
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Best Local Sin
Matches 155;
                                                            9446
                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A gene encoding a cellulose synthetic equipment - in the amount of cellulose synthesised in a plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1511
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                                                                                                                                                                                                                                                                                                               Sequence 10732 BP; 3149 A; 1212 C; 2074 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 14-21; 32pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-342371/30.
P-PSDB; AAY85179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MIZU/) MIZUNO K. (OJIP ) OJI PAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA10594 standard; DNA; 10732
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                                                                                                                                                                       h 3.3%; Score 57; DB 21;
Similarity 13.4%; Pred. No. 0.00015;
55; Conservative 451; Mismatches 525
                                                                                                                                                                                                                                                                                                                                                                   be used to improve by a plant.
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Best Local Similarity
Matches 173; Conserv
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                                                                                                                                                                                                                                                                                                                    The sequence is that of an example randomising oligonucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also AAQ21830-Q21832.
                                                                                                        1376
1496 atggttcgcaccaacggtggcaagcagtttgatgacatgagcatcgagctgaacggcatc 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New method of systematic polypeptide evolution by reverse translation - by linking each polypeptide in sample mixt. to individualised mRNA allowing further synthesis of selected
                                                                                                                                                                                                                                                                                                 Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ21833 standard; DNA; 390
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                                         cagctcaacgccaacactcacttgaaaattcgacaacttcaaggccgacgatttcggcacg
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                                                                                                                             polypeptide evolution by
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                        SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune mice which are the fl progeny of a cross of NZB and NZW parents CC (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope CC consists of ca. 10 amino acids at the N-terminus of the histone H2B CC protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a 77 promoter sequence and a ribosome binding CC site which is recognised by both prokaryotic and eukaryotic ribosomes, CC terminating in a restriction endonuclease site is synthesised and cloned CC using a number of oligonucleotides (example shown). A 3' fixed sequence is placed into a restriction site to provide an mRNA encoding the C-CC terminal trailer sequence of ca. 100 nucleotides lacking stop codons. CC In addition, a 3' primer annealing site is provided so that CDNA Synthesis can be accomplished on the mRNA recovered from partitioned CC ribosome complexes. See also AAQ36845-63.
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Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Systematic peptide evolution by reverse translation; specific; inhibitors; probes; assay; cell sorting; ss
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                                                                                                                                                                                                                                                                             Example 1; Page 84; 98pp; English.
                                                                                                                                                                                                                                                                                                               molecule
                                                                                                                                                                                                                                                                                                                                          Systematic
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-076529/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ36859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYRE-) UNIV RES CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                        Pribnow D,
                                                                                                                                                                                                                                                                                                                            polypeptide evolution by reverse translation - used of polypeptide ligand specific for desired target
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RESULT 1
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02-AUG-1990;
01-AUG-1991;
                    The present sequence was used in an example illustrating an invention relating to a method for isolating a polypeptide ligand for a desired target molecule. The method involves synthesising a nucleic acid mixture comprising mRNA having translatable and non-translatable regions and a mixture of nucleic acid polypeptide copolymers, each comprising the mRNA having translatable copolymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRIB/)
(SMIT/)
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                                                                                                                                                                             Example; Column 39;
                                                                                                                                                                                                                                      Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures comprised of ribosome complexes or mRNA.polypeptide copolymers relative to their affinity to the target molecule.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-243412/25
                                                                                                                                                                                                                                                                                                                                                                                                      Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence containing a 120 repeat of ACG flanked by fixed fragments.
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TUERK C.
PRIBNOW D.
SMITH J D.
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                                                                                                                                                                                                                                                                                                                                                                                                      Tuerk C,
                                                                                                                                                                                                                         the target molecule
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90US-0561968.
91US-0739055.
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       its associated mRNA.
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                                                                                                      Key
                                                                                                                                                                                  Bacillus sp. strain KSM-P15; pectic acid lyase; protopectinase;
protopectin; polygalacturonic acid; detergent; cotton; surfactant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 390 BP; 125 A; 126 C;
                                                                                                                                             Bacillus
                                                                                                                                                                    cellulase; protease; bleaching agent;
                                                                                                                                                                                                                          Bacillus sp strain KSM-P15 pectic acid lyase encoding
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                                                                                                      Location/Qualifiers
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08-APR-1998;

98WO-JP01613

15-OCT-1998.

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RESULT 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a protopectinase having an optimum pH 7 or higher against protopectin and polygalacturonic acid substrates. Inclusion of protopectinase gives a composition that provides better removal of muddy soil, particularly from socks. The present sequence encodes pectic acid lyase from Bacillus sp. strain KSM-P15, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detergent composition containing protopectinase active at alkaline pH\ \ - on protopectin and polygalacturonic acid, provides better removal of muddy soil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hatada Y,
Shikata S,
17-JAN-2000
                                                       AAX89484 standard;
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09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a detergent composition which contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAOS ) KAO CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention. Pectic acid lyase exhibits protopectinase
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Suzumatsu
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(first entry)
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97JP-0091142.
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tsu A,
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Tsumadori M,
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Wada Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pectate lyase I; EC 4.2.2.2; pectin degrading enzyme; ATCC 14580; catalytic active domain; cellulose binding domain; CBD; operably linked; optimum activity; pH; detergent composition; yarn; cellulosic fibre; recycled waste paper; pulp; retting process; animal feed; wine; juice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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06-MAY-1998;
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                                                                                                                                                                                                                                  Sequence 666 BP; 205 A; 136 C; 178 G; 147
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                                                                                                                                                                          Local Similarity
gttcgagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcga
                                                                                                                  caatgtggtgaaagacaccatcaaggtcggcgctggcgcaggtctttgacggccacggcgc 1149
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DB; AAY28446.
                                                        aaccttcactgccgacaaatctatgggtaacggagaccagggcgaaaatcagaagcccat 1209
                                                                                                 cgaggtcgttcacaaaacgatcgtagtcgagaaaggccaaacgtatgacggaaaaggcaa 146
                                          gcggctgattgcaggtccggagctcggggacggcagccaacgcgaggatcaaaaaccgat
                                                                                                                                                           154;
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                                                                                                                                                            Conservative
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Pred. No. 9.9e-05;
0; Mismatches 127;
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                         This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
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                                                                                                                                                                                                                                   Sequence 538 BP;
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                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection
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Reed SG, Skeiky YAW,
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                  for diagnosis, treatment and prevention of tuberculosis
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            ggcggcggcacaccccactgcaacaggtggcggcagggtggcacacccactgcaacagg- 972
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ggcggcctcaccggtactggcggcaccggcggcagcggtggcaccggcggtgacggcggt
                                                    ggcgacggcggtgccggcggaacggcggcggcggcacgggcaccggcggcgac
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96US-0730510.
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Pred. No. 0.00023;
0; Mismatches 183;
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                                       tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                            sequences. The invention relates to methods and compositions diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble
                                                                                                                                                                         AAV44436. XP22 DNA was isolated from a M. tuberculosis strain genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                     This is the 3' region of DNA coding for an antigenic portion of Mycobacterium tuberculosis antigen XP22; 5' DNA is provided in
                                                                                                                                                                                                                                                               Claim 4; Page 186; 250pp; English.
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Reed SG, Skeiky YAW,
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Sequence 538
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96US-0729622.
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 81 A;
 182 C;
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Twardzik DR,
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Search completed: October 4, 2001, 22:25:43 Job time: 5894 sec

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2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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## ALIGNMENTS

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (gen
US-09-120-817-1
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APPLICANT: Charkowski, Amy
APPLICANT: Alfano, James R.
TITLE OF INVENTION: HYPERSENSITIVE
TITLE OF INVENTION: PSEUDOMONAS S)
TITLE OF SEQUENCES: 8
                                                                                                                                  TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION UMBER: US 60/055
APPLICATION NUMBER: US 60/055
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-Lease #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Box
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/120,817 FILING DATE:
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                          DNA (genomic)
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APPLICANT: Gold, Larry
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Ever Title Reference: NEXO2/C1 CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
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US-09-197-649-7
; Sequence 7, Application
; Patent No. 6194550
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FEATURE:
OTHER INFORMATION:
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                                                                                                       SOFTWARE: Pa
SEQ ID NO 1
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09402668 Patent No. 6172030
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Best Local Similarity 47.1%;
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OTHER INFORMATION: Strain: KSM-P15
NAME/KBY: CDS
LOCATION: (1)..(591)
-09-402-668-1
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: 9-242736 JAPAN
PRIOR APPLICATION NUMBER: 9-242736
                                                                                                                                       PRIOR FILING DATE: 1998
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                 APPLICANT: TSUMADORI, Masaki
TITLE OF INVENTION: Detergent Composition
FILE REFERENCE: 2173-0116P
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 9-24 PRIOR FILING DATE: 1997-09-08
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
                                                              FEATURE:
                                                                        ORGANISM: Bacillus sp
                                                                                           TYPE: DNA
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SHIKATA, Shitsuw
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KOBAYASHI, Tohru
                                                                                                                                                                                                                                                                                                                                                                                           KOIKE, Kenzo
                                                                                                                                                                                                                                                                                                                                                                                                               SUZUMATSU, Atsushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WADA, Yasunao
                                                                                                                                                                                                                                                                                                                                                 ITO, Susumu
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                                                                                                                                                                                       PCT/US98/01613
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Pred. No. 1.3e-05;
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; ORGANISM: Bacillus licheniformis
US-09-198-956-3
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                                                                         Query Match
Best Local Similarity
Matches 154; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 666
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Best Local Similarity 50.8%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andersen, Lene N.
APPLICANT: Schulein, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Pectin Degrading Enzymes TITLE OF INVENTION: Licheniformis
                       1090 caatgtggtgaaagacaccatcaaggtcggcgctggcgcaggtctttgacggccacggcgc 1149
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cyaggtcgttcacaaaacgatcgtagtcgagaaaggccaaacgtatgacggaaaaggcaa 146
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                                                                                    Conservative
                                                                                                      3.2%;
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Pred. No. 1.6e-05;
0; Mismatches 199;
                                                                                                      Score 55.8; DB 4;
Pred. No. 2.6e-05;
                                                                                    Mismatches
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US-08-232-463-14
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                                  Matches
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Patent No.
                                                Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
1214 gagctggctgaaggcgctacgttgaagaatgtgaacctgggtgagaacgaggtcgatggc 1273
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/ARENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REGISTRATION NUMBER: 30472/114 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                  . Similarity
20; Conserv
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(703)683-4109
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DORNER, F.
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                               Score 53.6; DB 1
Pred. No. 0.00024;
17; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5958764
                                INFORMATION FOR SEQ ID NO:
                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1274
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                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect (Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/146,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                               FILING DATE: October 29, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE: April 30, 1992
APPLICATION NUMBER: NO. 5958764 yet assigned (204/132)
                                                TELEFAX: (213)
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 90017
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 611 West
CITY: Los Angeles
                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                 NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggcaagcagtttgatgacatgagcatcgagctgaacggcatcgaagctaaccacggcaag 1573
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6530 bases
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                                                                                                                                                                                  October 29, 1993
                                                                 955-0440
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: described below:
07/876,286
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/146,930
FILING DATE:
APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
FILING DATE: October 29, 1993
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTMARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: DNA (9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.:
TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3834 TCCTCTGGCGGCGGTGGCGGCGGTGGCTGCTACTCCAGCGGTGGTGGCGGCAGCAGCGGT 3893
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                                   TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
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STATE: California
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Pred. No. 0.0022;
D; Mismatches 117;
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GENERAL INFORMATION:
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                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
APPLICATION NUMBER: PCT/US
FILING DATE: 19930428
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,71
          TOPOLOGY: 111641
MOLECULE TYPE: DNA
MOLECULE TYPE: NO
ANTI-SENSE:
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 77010-3095
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                                                                                NUCLEIC
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                                                                                6530 base pairs
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1301 McKinney, Suite 5100
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Greenhalgh, David A.
Greenhalgh, David A.
VERTION: CONSTITUTIVE AND INDUCTBLE EPIDERMAL
VENTION: VECTOR SYSTEMS
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                              DNA (genomic)
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Pred. No. 0.0022;
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; ORGANISM: Mycobacterium tuberculosis
US-09-177-349-2
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Best Local S
Matches 120
                                                       Sequence 4, Application US/09060756 Patent No. 6183957 GENERAL INFORMATION:
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Best Local Similarity
Matches 111; Conserv
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LENGTH: 5036
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APPLICANT: Jacobs Jr., William R.
APPLICANT: Jacobs Jr., William R.
APPLICANT: TNUFNUTION: iniB, iniA AND iniC GENES OF MYCOBACTERIA AND METHODS
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch,
APPLICANT: Gordon, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/177,349
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 0.0022;
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US-08-118-200-1
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Best Local Similarity 53.3
Matches 100; Conservative
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CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
FILING DATE: 09-SEP-1993
CLASSIFICATION: 435
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APPLICANT: SUTHER
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                         COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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APPLICANT:
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CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                             PRITCHARD, Melanie April
LYNCH, Michael
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MULLEY, John C
MANDEL, Jean-Louis
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NAGARAJA, Ramaiah
                                                                       PatentIn Release #1.0, Version
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Robert I
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Pred. No. 0.0054;
0; Mismatches 8
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 05-DEC

NUMBER: US 07/802,650 05-DEC-1991

APPLICATION NUMBER: FILING DATE: 20-MA

20-MAR-1991

US 07/672,232

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Best Local Similarity 56.0
Matches 89; Conservative
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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                                                                                      NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
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REFIRENCE/DOCKET NUMBER: 020160-164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 336-6620
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                                                                                                                                        TITLE OF INVENTION:
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COMPUTER READABLE FORM:
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                COUNTRY: United ZIP: 22313-1404
                                                            CITY: Alexandria
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                                                                             STREET:
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                                             Virginia
                                                                             P.O. Box 1404
                               United States
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MANDEL, Jean-Louis
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Pred. No. 0.0056;
0; Mismatches 70;
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US-08-762-106-5
; Sequence 5, Application US/08762106
; Patent No. 5948677
; PATENTIAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: US 0.
FILING DATE: 04-JAN-1991
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 1028 base pair
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 23-DEC-1992
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                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                862 aggcggtggcggcggtgatactccgaccgcaacaggcggtggcggcagcggtggcggcgg 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 CGGCGGCGGCGGCGGCGGCGGCCCGGAGCCACC
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OPERATING
SOFTWARE:
                                              COUNTRY:
                                                                STATE:
                                                                                 CITY:
                                                                                           ADDRESSEE: Harris Brotman STREET: 202 Coast Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 20-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 09-SEP-1993
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                                  ZIP:
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                                  92037
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                                                                               La Jolla
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Floppy disk
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READING FRAME INDEPENDENT EPITOPE
TAGGING
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Pred. No. 0.0056;
Pred. No. 70;
                                                                                              Suite 111
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CURRENT APPLICATION DATA:

OPERATING SYSTEM: SOFTWARE: Patent

PatentIn Release #1.0, Version #1.25

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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Best Local Similarity
Matches 101; Conserv
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APPLICANT: Jarvík
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APPLICATION NUMBER: US/01
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Profite Harris F
                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1303 CCGCCGGCGGAGC 1315
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LENGTH: 1548 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                      CURRENT APPLICATION DATA:
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                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brotman, Harris F. REGISTRATION NUMBER: 35,461
                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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La Jolla
California
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TAGGING
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Pred. No. 0.013;
Prematches 92;
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                                                                                   Version
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                                                                                                                                                                               Query Match
Best Local Similarity
Matches 101; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                     LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                  23789 gggcggctgatgcaggggctctcggcggggcggcggcgatggtgtcgctcggagcgccggag 23848
                                               23849 gcggaggtggcggcggtggcgccgcacgcggcgtcggtgtcgatcgcggcggtcaat 23908
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                                                                                                                                       804 ggggcggcggtacaccggatgcgacaggtggcggcggtgatacgccaagcgcaacag 863
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924 cacccactgcaacaggtggcggcaggcggtggcacaccccactgcaacaggcggtggcgagg 983
                                                                    864 gcggtggcggcggtgatactccgaccgccaacaggcggtggcggcagcggtggcggcggca 923
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Pred. No. 0.12;
0; Mismatches 94;
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Db 23909 gggccggagcaggtggtgatcgcgggcgtggagcaagcggtgcaggcgatcgcggcgggg 23968

Qy 984 gtggcgtaacaccgc 998 | | | | | | | | | | | | | | | 23969 ttcgcggcgcgcgc 23983

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Minimum
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Listing first 45 summaries
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length: 2000000000
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9b\_est48:\*
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9b\_est53:\*
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9b\_est66:\*
9b\_est100:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

genome

of the

Fisher, C.,

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48.4
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Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 681)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
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262H14 of
                                                                                                                                                     sequence.
AL193990
AL193990.1 GI:7832096
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AW564035 LG1_281_D

BG355552 EM1_17_G1

AL254315 Tetraodon

AL106698 GH07623.5

BG444367 GA_Ea002

AW729119 GA_Ea002

AW729119 GA_Ea002
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BG054210 OV2_2_G10
AL538536 AL538536
BE214873 HV_CEb000
AU172673 AU172673
BE494156 WHE1251_E
AU089814 AU089814
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AL104839 Drosophil
AW702254 TgEST2574
BG417399 HVSMEK001
AL1065629 Drosophil
AL109292 Drosophil
AL109292 Drosophil
AL333308 SD05070.5
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AL310686 Tetraodon
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AI533308 9
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide anal
Tetracdon nigroviridis DNA sequence
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Charaterization and repeat analysis of the control of t
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Direct Submission
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nilarity 43.1%;
Conservative 17
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/db_xref="taxon:99883"
/clone="162H14"
/clone_11b="G"
/clone_11b="G"
/clone_11b="G"
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Pred. No. 0.00011;
7; Mismatches 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acaggcggtggcggcagcggtggcggcacaccccactgcaacaggtggcggcagcggt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99c999ctc99tacacc9tc99cc9atagc99999gc9gcggtacaccggatgcgacaggt 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTTAATTGTTGGTGGTGGTGGTGGCGGTGGCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118;
   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes
Tetraodontidae; Tetraodon.
1 (bases 1 to 630)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                          Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS04HMV 630 bp DNA GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
110F12 of library G from Tetraodon nigroviridis, genomic survey
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                             AL291136.1
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University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 421 row: H column: 7 High quality sequence stop: 525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.fruitfly.org/EST, Plate: 421 row: H column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Harvey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpubl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Art
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="%XL1 Blue"
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/db_xref="taxon:7227"
/clone="LD42191"
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Pred. No. 0.00016;
0; Mismatches 102;
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                                                           Dasilva, C., Fizames, C., Fisher, C
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RESULT 4
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                                                                                                                                                       AL053013.1
GSS.
                                                                                                                                                                                                                        CNSUUYIP 925 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19D16 of RPCI-98 library from Drosophila melanogaster (fruit
Direct Submission Submitted (02-JUN-1999)
                                    Genoscope.
                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilldae; Drosophila. 1 (bases 1 to 925)
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                                                                                                                                                                                           fly), genomic survey sequence. AL053013
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                                                                                                                                         fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome. For more information, please thitp://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ This sequence is a single read and was generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="110F12"
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Indels Length 327;

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 327)
                                                                 Unpublished (2000)
                                                                                     Sasaki,T. and Yamamoto,K. Rice cDNA from green shoot (2000)
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                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/db_xref="taxon:7227"
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/clone="BACR19D16"
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                                                                               BP 191 91006 EVKI CELLER

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant avec Pavan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence T7 end of BAC BACN13L17 of DrosBAC library from Drosophila melanogaster (fruit
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Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1034)
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/note="Green shoot (8 days old)"
54 c 180 g 58 t
  /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
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/db_xref="taxon:4530"
/clone="S16719"
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81; Conservative
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Tel: 919 613 8164
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Elizabeth H. Harris
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Location/Qualifiers
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/clone_lib="DrosBAC"
/clone="BACN13L17"
/note="end: T7"
a 256 c 236 g
              mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. FOLYA MRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5'y and XhoI (3') sites. pBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with EXASSIST (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                            XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                                                                                                       /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db.xref="taxon:3055"
/clone_11b="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK-; Site_1: EcoRI;
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892 aacaggcggtggcggcagcggtggcggcacccactgcaacaggtggcggcagcgg
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                                                                                                                           gcggtggcacacccactgcaacaggcggtggcgagggtggc
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                                                                                                                                                                                                               VRGGRVCCAGGGASCACMAADCGGCCAKMACCSSSSASSSGSSCASTSSSASRGGMVSSC 742
                                                                                                                                                                                                                                                 ACAGCAGCGGCCACGGCGTTGGGCCCGGTGGTGGTGGCGGC
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59; Conserv
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain) with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with finding provided by a MRC d'Etude du Polymorphisme Humain with f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence. AL108460
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176 c 160 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                          Score 50.6; DB 219;
Pred. No. 0.009;
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Pred. No. 0.0072;
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                                                                                                                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovegenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                             Characterization and repeat analysis of the compact freshwater pufferfish tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crollius, H.R., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Boune Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome using Tetraodon nigroviridis DNA sequence using Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL310686.1 GI:9543554
GSS; genome survey sequence.
Tetraodon nigroviridis.
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/note="Genoscope sequence
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196 c 342 g 234
                                                                                                                                                            /clone="052H06"
                                                                                                                                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Score 50; DB 22
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end of clone
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nigroviridis
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cccactgcaacaggtggcggcagcggtgg
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                                                                       ggtggcggcggtgatactccgaccgcaacaggcggtggcggcagcggtggcggcggcaca
                                                                                                          GGAGGCGGCGGATCCGGTGGTGGCGGACACAGCGGCCGCCATCATGGAGGCGGATGTGGC
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WS1_37_C06.g1_A002
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Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                             /clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
101 c 161 g 130 t
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/db_xref="taxon:4558"
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Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                AGCCAACTGGTGGAAAGCGGTCCTGATACCTACGCTCCAACTAGTGGCAACAGCAACA 402
                                                                                                                                                                           BF621686 824 bp mRNA EST 21-FEB-2001
HVSMEa0011N20f Hordeum vulgare seedling shoot EST library
                                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 541)
Cliften, P.F., Hiller, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces kluyveri
Saccharomyces kluyveri
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Eukaryota; Fungi; Ascomycotaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ928169 541 bp DNA GSS 01-APR-2001
479.dif05d06.s1 Saccharomyces kluyveri Saccharomyces kluyveri
genomic clone 479.dif05d06.s1, DNA sequence.
                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Hordeum.
                                                                                                                                   mRNA sequence.
BF621686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University Medical School
Box 832, 4566 Scott Ave., St. Louis
Tel: 314 362 7785
Fax: 314 362 7855
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                                                                       Hordeum vulgare
                                                                                                                                                               HVcDNA0001 (Cold stress) Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Johnston M
                                                                                       barley.
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              (bases 1 to
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135 c 168 g 158 t
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/clone_lib="Saccharomyces kluyveri"
/clone_lib="Saccharomyces kluyveri"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"
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                                                           Nomoto,H
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditic
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 180)
1 (bases 1 to 180)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki
Nishigaki,A., Motohashi,T., Zeng,Q., Wangitu Sugimoto,A.,
Nishigaki,A., Motohashi,T., Zeng,Q., Thierry-Mieg,D., Witsuki
                                                                                                                                                                                                                                                                                                                                                         AV199870 180 bp mRNA EST 26-JUL-1999
AV199870 Yuji Kohara unpublished cDNA Caenorhabditis elegans
clone yk552h11 3', mRNA sequence.
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Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
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Clemson University
100 Jordan Hall, Clemson, SC
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Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                               AV199870
AV199870.1 GI:5583641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288 Fax: 864 656 4293
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                                                                                              Miyata, A., Mitani, Y., Iida, K.,
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HVcDNA0001 (Cold stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: Ecc
a 257 c 264 g 142 t
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/db_xref="taxon:4513"
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                                                                                                Uesugi, H., Sugiyama, Y. and
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Eukaryota; Metazoa; Nematod
; Rhabditidae; Peloderinae;
                                                                                                                                                                                                              Yata 1111, Mishima, Shizuoka 411, Tel: 81-559-81-6854
                                                                                                                                                                                                                                                                 Contact: Yuji Kohara
Gene Library Lab
                                                                                                                                                                                                                                                                                                Expressed genes in C.elegans Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                 Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M.,Miyata,A., Mitani,Y., Ilda,K., Uesugi,H., Sugiyama,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV175960
AV175960.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV175960 300 bp mRNA EST 21-JUL-1999 AV175960 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk499c4 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4.
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                               National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                        Nomoto,H
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                                                                                                                                                                                            81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ykohara@lab.nig.ac.jp
Location/Qualifiers
                                                                                                                                                         ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ည
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole animal"
/dev_stage="varied"
96 c 20 g 32 t
                                                                                                      /strain="N2"
                                                    /clone_lib="Yuji Kohara unpublished
                                                                       /clone="yk499c4"
                                                                                         /db_xref="taxon:6239"
                                                                                                                        organism="Caenorhabditis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Yuji Kohara unpublished
/sex="hermaphrodite, male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="yk552h11"
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derinae; Caenorhabditis.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cggtggcacacccactgcaacaggcggtggcgagggtggcgtaacac 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgcaacaggcggtggcggcagcggcggcacacccactgcaacaggtggcggcag 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTGGTGGCGGCGGTGGCTATGGAAGCGGTGGAGGATGGGGTGGCGGCGGTGGCGGCAG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI058502 343 bp mRNA EST UI-R-C1-kv-d-01-0-UI.S1 UI-R-C1 Rattus norvegicus UI-R-C1-kv-d-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through Research Genetics This clone is also available thro
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1784479 The following repetitive elements were found in
cDNA sequence: 30-75, >(TGG)n#Simple_repeat 124-210, >(CGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction: two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
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Similarity 54.5%;
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                   /lab_host="PHIOB (Life Technologies)"
/lab_host="PHIOB (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note:-pT/T3D-Pac (Pharmacia) with a modified
/note:-pT/T3D-Pac (Pharmacia) with a modified
/note:-pT/T3D-Pac (Pharmacia) with a modif
consisted of a mixture of individually libraries constructed from rat placenta,
                                                                                                                                                                                                                                                                       /organism-"Rattus norvegicus"
/Strain-"Sprague-Dawley"
/db_xref-"taxon:10116"
/clone="UJ-R-C1-kv-d-01-0-UJ"
/clone_11b="UJ-R-C1"
                                                                                                                                                                                                                                          /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
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Pred. No.
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Query Match 2.8%;
Best Local Similarity 55.6%;
Matches 94; Conservative
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                                                                                                                                                                   816 caccggatgcgacaggtggcggcggcggtgatacgccaagcgcaacaggcggtggcggcg 875
148 GTGGTCCGGGCAGCGCGGGGGGGGGGGGGGGGGGAC 196
                                                                                                                                 brain, liver, kidney, heart, spleen, ovary, and muscle. The UIR-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"
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BASE COUNT

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Listing first 45 summaries
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AAB23357	AAR94895	AAW74574	AAW18573	AAW74575	AAW00926	AAW68207	AAY04999	AAG36618	AAG36619	AAG36620	AAW68201	AAG51723	AAB66103	AAB31205	AAB87551	AAY99354	AAW31853	AAY84860	AAY71099	AAW87641	AAW61116	AAW62457	AAW75865	AAW06600	AAR05877	AAW68203	AAB70182	AAG29727	AAG29728	AAY95556	AAY95559	AAW68205	AAP70709
_	trophinin.	Human cyclin D1/cy	cyclin D1	Human cyclin D1/cy		M. catarrhalis str	Mycobacterium spec			Arabidopsis thalia	$\mathbf{L}$	Arabidopsis thalia		Amino acid sequenc	11.	Human PRO1411 (UNQ	Mycobacterium tube	A hypersensitive r	Pseudomonas solana	A hypersensitive r	Hypersensitive res	Pseudomonas solana	Pseudomonas solana	Hypersensitive res	Merozite surface a	M. catarrhalis str	Peptide dendrimer	Arabidopsis thalia		Caenorhabditis ele	Caenorhabditis ele	M. catarrhalis str	Plasmodium cynomol

## ALIGNMENTS

RESULT AAW97851 Region 06-AUG-1997; 24-JUL-1998; Domain Key Hypersensitive response elicitor; dspE gene; HrpW; transgenic plant; disease resistance; insect resistance Hypersensitive response elicitor HrpW. 07-JUN-1999 (first entry) AAW97851 standard; Protein; 424 AA (CORR ) CORNELL RES FOUND INC 18-FEB-1999. WO9907207-A1. AAW97851; Domain Pseudomonas syringae pv. tomato 97us-0055107. 98WO-US15501. 119..186
/note= "region of 6 imperfect glycine-rich repeats"
187..424 /note= "hypersensitive response elicitor-like
 domain" Location/Qualifiers
1..186 /note= "C-terminal domain"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 424;
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AAY71098;
                            AAY71098 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hypersensitive response eliciting (dspE) gene and protein useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 25-26; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application of a hypersensitive response
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                                                                                                                                                                        ptatgggeggvtpqitpqlanpnrtsgtgsvsdtagsteqagkinvvkdtikvgagevfd
                                                                                                                                                                                     PTATGGGEGGYTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFD
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                                                                                                                                                                                                                                                                        dstvqnpqdaskpndsqsniaklisalimsllqmltnsnkkqdtnqeqpdsqapfqnngg
                                                                                                                                                                                                                                                                                      DSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGG
                                                                                                                                                                                                                                                                                                                       MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen;
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Pred. No. 7.5e-155;
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Best Local S
Matches 424
                                                                                                                                                                                                                                                                   may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, calliflower, broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a hypersensitive response elicitor polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants especially vegetables and ornamental flowers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 26-28; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A hypersensitive
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                                                                                         MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGTP 60
 LGTPSADSGGGGTPDATGGGGGDTPSATGGGGGGDTPTATGGGGSGGTPTATGGGGSGGT
                             dstvqnpqdaskpndsqsniaklisalimsllqmltnsnkkqdtnqeqpdsqapfqnngg
                                                DSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGG
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                                                                                                                                                          Score 2200; DB 21;
Pred. No. 7.5e-155;
Mismatches 0;
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                      The hypersensitive response eliciting protein (hrp) or polypeptide is produced as part of an active defense by plants against incompatible pathogen infections. The hypersensitive response is a rapid localised necrosis. The hrp protein and gene when used in nucleotide constructs are useful for providing disease resistance t plants, insect control to plants, and enhancing plant growth (enhancing fruit size and earlier colouration and maturation), by direct application of the protein to plants, or by producing transgenic plants or seeds using the hrp gene.
                                                                                                                                                                         New Erwinia amylovora hypersensitive response eliciting gene an protein - useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
                                                                                                                                                  Claim 1; Page 50-51; 54pp;
                                                                                                                                                                                                                                          WPI; 1999-167126/14.
                                                                                                                                                                                                                                                                   Beer SV,
                                                                                                                                                                                                                                                                                                                     06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pest resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrpW; pathogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               infection; crop protection; transgenic plant; colourat
                                                                                                                                                                                                                                                                                            FOUND INC
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                                                                                                 The hypersensitive response is a
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The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a hypersensitive response elicitor protein from Erwinia amylovora. The protein is
                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor; plant.
                                                    Disclosure; Page 10-12;
                                                                       Application of a hypersensitive response elicitor protein impart stress resistance
                                                                                                                                      Wei Z,
                                                                                                                                                                                                 04-NOV-1999;
                                                                                                                                                                                                                                          WO200028055-A2
                                                                                                                                                                                                                                                              Erwinia amylovora
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                                                    84pp; English.
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                                                                                                  N-PSDB; AAA14939.
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Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plant: especially vegetables and ornamental flowers -

plants

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental
                            WO9845393-A2
                                                                                    Bacillus sp.
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                                                                                                                                                                                                                                                                   Bacillus sp strain KSM-P15 pectic acid lyase.
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Pred. No. 1.6e-33;
54; Mismatches 132;
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RESULT
AAW77412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hatada Y,
Shikata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a detergent composition which contains a protopectinase having an optimum pH 7 or higher against protopectin and polygalacturonic acid substrates. Inclusion of protopectinase gives a composition that provides better removal of muddy soil, particularly from socks. The present sequence represents pectic acid lyase from Bacillus sp. strain KSM-P15, which is used in an example from the present invention. Pectic acid lyase exhibits protopectinase
                                                                                                                                                                                                           AAW77412 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detergent composition containing protopectinase active at alkaline pH - on protopectin and polygalacturonic acid, provides better removal of muddy soil
                                                                                       Bacillus sp. detergent; for
                                                                                                                               Bacillus
                                                                                                                                                      07-JAN-1999
                                                                                                                                                                                   AAW77412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity
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N-PSDB; AAV69879.
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09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-1998;
                                                             Bacillus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 71-72; 80pp; English.
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                                                                                                                                                                                                                                                                                                      405 MT 406
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                                                                                                                                                                                                                                                                                                                                                                                                285 GIHVKAKNAQEVTIDNYHAQNYGEDLITYKGEGGAAVTNLNIKNSSAKGADDKYVQLNAN 344
                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                  4 vvhetirvpagqtfdgkgqtyvanpntlgdgsqaenqkpifrleagaslknvvigapaad
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                                                                                                                                                                                                                                                                                                                            gtinirnfraddigklvrqnggtty-kvvmnvencnisrvkdailrtds---ststgriv
                                                                                                                                                                                                                                                                                                                                                                                 gvhcyg----dctitnviwedvgedaltlkssg----tvnisggaaykaydkvfqinaa
                                                                                                                                                                                                                                                                                                                                                       THLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIA 404
                                                                                                                             sp.
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Suzumatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                      b. KSM-P15; pectic acid lyase; pectinic acid lyase; pectin; food-processing; fibre-processing agent; cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                       (first entry)
                                                                                                                             pectic acid lyase.
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97JP-0091142.
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tsu A, Tsumadori M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 318; DB 19; 40.7%; Pred. No. 3.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
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5

14-OCT-1998

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RESULT
AAX/284
ID AAY2
XX AAY2
XX AAY2
XX Baci
DE Baci
XX Baci
XX Pect
KW Pect
KW Optil
KW recy
KW tran
XX ITAN
XX ITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a pectic acid lyase isolated from microorganism Bacillus sp. KSM-P15. The pectic acid lyase has high pectic acid lyase activity which degrades pectin in plant cell walls and fibre in vegetables, and so is useful as a component of detergents, a food-processing agent, or a fibre-processing agent. The pectic acid lyase has a higher optimum reaction pH (10.3-10.7) than known Bacillus pectic acid lyases (pH 8-9.5) and so has wider industrial applications. Unlike present pectic acid lyases, the new enzyme has a high enzyme
                                                                                                                                                                                          Pectate lyase I; EC 4.2.2.2; pectin degrading enzyme; ATCC 14580; catalytic active domain; cellulose binding domain; CBD; operably linked; optimum activity; pH; detergent composition; yarn; cellulosic fibre; recycled waste paper; pulp; retting process; animal feed; wine; juice;
                         Peptide
                                                                                                                Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis Pectate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28446 standard; Protein; 221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 16-17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Bacillus pectic acid lyase - useful as a food-processing agent and a fibre-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1997;
09-APR-1997;
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                                                                                                                                                                      transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, and can be produced on a mass scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hatada Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|vvhetirvpagqtfdgkgqtyvanpntlgdgsqaenqkpifrleagaslknvvigapaad|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gvhcyg----dctitnviwedvgedaltlkssg----tvnisggaaykaydkvfqinaa
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97JP-0091142.
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1..27
/label= Pro-sequence
                                                         Location/Qualifiers
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40.7%;
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Pred. No. 3.5e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzumatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 197;
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RESULT 1

10

BXBXEXB

AAG29582;

AAG29582 standard;

Protein;

730

B

17-OCT-2000

(first entry)

Arabidopsis thaliana protein

fragment SEQ ID

NO:

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                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                       The present sequence is pectate lyase I, which is a pectin degrading enzyme derived from Bacillus licheniformis, ATCC 14580. The enzyme comprises a catalytic active domain and a cellulose binding domain (CBD) that are operably linked to each other. It shows optimum activity at pH greater than 9 and temperature 55 degree centigrade. It can be use in detergent compositions, for cleaning hard surfaces, for machine treatment of fabrics, for improving the properties of cellulosic fibres, yarn, woven or non-woven fabric, for the degradation of plant material e.g. recycled waste paper, mechanical paper-maxing pulps or fibres subjected to retting process, for preparing animal feed and for processing wine or juice. DNA encoding the enzyme can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1998;
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189 stssvtmtntryskvgqkwigvkhater 216
                             399
                                                                                                                                            279
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                                                                                                                84
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                             ATGNIAMTD-
                                                       fqinkastftvknftadqggkfirqlggstfkav-vnidnctitnmkeaifrtds----
                                                                                   VQLNANTHLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKL
                                                                                                              gapaadgvhtyg----nasinnvvwedvgedaltvkseg----svtinggsarlaadki
                                                                                                                                          GENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKV 338
                                                                                                                                                                     ekalaaevvhktivvekgqtydgkgkrliagpelgdgsgredgkpifkvedgatlknvvl
                                                                                                                                                                                                  EQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-610578/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Page 79-80; 93pp; English.
                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                Conservative
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98US-0073684
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155
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/label= Mature_pectate_lyase_I
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                              13.4%; Score 294.5; DB 20 34.6%; Pred. No. 2.2e-14; tive 38; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ME,
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                            -VKHAYDK 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue"
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                                                                                                                                                                                                                                                          20;
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                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schuelein
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29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
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13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
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01-SEP-1999;
07-SEP-1999;
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07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                             180
  302 HAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMV
                                                      338
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                                                                                                                                                                              ---GGYTPQITPQLANPNRTSGTGSVSDTAGSTEQ----AGKINVVKDT-IKVGAGEVFDG
                                                                                                                                                                                                                                                                               GG------GGDTPSATGGGGGDTPTATGGGGSGGGG---TPTATGGGSGGTPTATGGGE
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                                                 nggtndgasgigsndgstgtnpg---agggtdsniegtennvggket-----np
                                                                                                HGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNV
                                                                                                                                                 snagg-----sksndganngasgiesnagstgtnfgaggtggigdtesdaggsktnsg
                                                                                                                                                                                                                                                                                                                                                        tnpgasa-----vgngeteknaggskpss----gsagtnpgasaggngeteknv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGT---PDSTVQNPQDA--SKPNDSQSN 79
                                                                                                                                                                                                                                                    ggskpssgkagtnpganaggnggteknaggsksssgsartnpgasaggngetvsnigdte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 215; DB 21; ilarity 24.0%; Pred. No. 8e-08; Conservative 46; Mismatches 180;
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990S-0154038
990S-0154779
990S-0155486
990S-0155486
990S-0155659
990S-0156596
990S-0157117
990S-0157117
990S-0157865
990S-0158029
990S-0158029
990S-0158369
990S-0159294
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990S-0160980
990S-0160980
990S-0161404
990S-0161406
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990S-0161350
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990S-0161351
990S-0161920
990S-0161993
990S-0161993
990S-0161993
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990S-0159584.
990S-0160741.
990S-0160767.
990S-0160767.
990S-0160760.
990S-0160770.
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99US-0151930.
99US-0152363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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RESULT 11
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AAG29581 standard; Protein; 752
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                                                                                                                                                                                                                                                  EP1033405-A2
                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                   termination sequence.
                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2000
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
99US-0128714.
99US-0129845.
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Query Match
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16-AUG-1999
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27-AUG-1999
28-EP-1999
28-EP-1999
29-SEP-1999
20-SEP-1999
21-SEP-1999
21-SEP-1
2h 9.8%;
| Similarity 24.0%;
| 99; Conservative
                                                             9908-0148341
9908-0148684
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9908-0149930
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9908-0161360
9908-0161360
9908-0161361
 ; Score 215; DB 21;
; Pred. No. 8.3e-08;
46; Mismatches 180;
                                 Length
   Indels
   88;
 Gaps
      17;
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16-JUN 1999
17-JUN 1999
18-JUN 1999
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9908-0139452
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RESULT 12
AAP70709
ID AAP7077
XX AAP7077
XX DT 01-JAN
XX Immuno
XX Immuno
XX Immuno
XX Plasmo
XX Plasmo
XX VORTO
PN WO8700
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PN WO8700
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XX PLASMO
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Query Match
Best Local S
Matches 60
                                                                                                                                                                                                              The gene encoding the circumsporozoite protein of P. cynomolgi is used during the detection of the circumsporozoite protein of P. vivax. A DNA probe from this P. cynomolgi sequence, designated P236-7, is useful in the construction of an anti-malarial vaccine.
                                                                                                                                    Sequence
                                                                                                                                                                                          See also
                                                                                                                                                                                                                                                                                                                                                        Disclosure; fig. 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New Plasmodium vivax circumsporozoite protein - and peptide(s) contg. its dominant epitope, useful in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN71065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNY-) NEW YORK UNIV.
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                                                  Score 201;
                            Pred.
Mismatches
                         No. 4e-07;
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                                                  DB 8;
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anti-malarial
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RESULT 13
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                          CC Nucleic acid sequences encoding the UspAl and A2 antigens of Nucleic acid sequences encoding the UspAl and A2 antigens of CC M. catarrhalis isolates 0355, 0465, TMA24 and TTMA7 can be used in CC genetic vaccination. An antigenic composition or vaccine containing antigenic peptides from UspAl or UspA2 antigens are used to induce an CC immune response in mammals against M. catarrhalis and can be used to treat infections such as otitis media, sinusitis, lower respiratory CC treat infections such as otitis media, sinusitis, lower respiratory CC tract infections. They can also be used as immunity enhancers for other CC bacterial, parasitic or viral antigens, to raise antibodies and as immunity enhancers for other CC constitution of the epitopic core sequence, by immunoassay reagents. CC Detection of the epitopic core sequence, by immunoassay or by PCR, is used to diagnose infection. The Usp antigens encoding nucleic acid sequences are also used to produce recombinant proteins and for screening constitution and interest accordance.
                                                                                                                                                                                                                                                                                                                                                               New peptide(s) containing the core epitope of Moraxella catarrhalis Usp proteins - useful in, e.g. vaccines to prevent or treat M. catarrhalis infection, and antibodies for passive immunisation \frac{1}{2}
                                                                                                                                                                                                                                                                                                                              Claim 30; Pages 152-155; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-377595/32.
N-PSDB; AAV41345.
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Maciver I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis; UspAl; UspA2; antigen; genetic vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. catarrhalis strain TTA24 UspAl antigen
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               useful as diagnostic probes or primers or to isolate variant sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; otitis media; sinusitis; lower respiratory tract infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunity enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 yldki 329
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RESULT 1
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ID AAY9
XX AAY9
AC AAY9
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XX Loca
KW Polly
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location of vulva; LOV-1 gene; nematode; mating behaviour; polycystin; polycystic kidney disease; animal model; signal transduction; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
   Example 1; Page 131-139; 142pp; English
                                                                                                   producing tr
identifying
                                                                                                                                                                                                                                              WPI; 2000-452537/39
                                                                                                                                                                                                                                                                                                             Sternberg PW, Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-1999;
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                                                                                                   Isolated nucleic acid molecules from Caenorhabditis elegans useful for producing transgenic nematodes with altered mating behavior for identifying genes or regulatory factors involved in polycystic kidney
                                                                                                                                                                                                                                                                                                                                                                                 (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 GNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ATGGGS-----GGTPTATGG-----GE-----GGVTPQITPQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 8.2%; Score 179.5; DB 19; Length
Local Similarity 25.0%; Pred. No. 4.7e-05;
ses 97; Conservative 39; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---MSIELNG----IEANHGKFALVKSD 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v-gagqisatstdavngsqlhalakavakn---
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The present sequence is that of a deletion allele, termed lov-1(sy582del), of the Caenorhabditis elegans LOV-1 protein (see AAY95556), generated by genomic deletion of the PKD/channel domain of the lov-1 gene by PCR. LOV-1 is an orthologue of the human polycystin-1 (PKD1) gene that is defective in human autosomal dominant polycystic kidney disease (PKD). The LOV-1 autosomal dominant polycystic kidney disease (PKD). The LOV-1 protein is involved in chemosensory or mechanosensory signal transduction in sensory neurons. It is required for 2 male sensory behaviours, 'response' of males to hermaphrodites, and 'location' of the vulva. Nematodes such as C. elegans that express mutant or wild-type LOV-1 or PKD-2 (see AAY95557) can be used to study the functions of the proteins encoded by these genes, to screen for other genes involved in PKD, to identify mutations
                                                                           screen for other genes involved in PKD, to identify mutations involved in the disease, and to screen for drugs that affect PKD. Behaviours controlled by the action of the genes or gene products are identified and used in the assays. Hence, an animal model is provided that permits study of the etiology of PKD and provides a tool to identify the genes involved in the disease pathway, to identify compounds that may be used to treat or after the disease
Sequence
                                                         progression,
   2870 AA;
                                                         lessen its severity or ameliorate symptoms.
                                                                                                                                                                                                                                                                                                                             can be used
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Matches
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Best Local Similarity
1497 mat 1499
                                                                                       1437 iyltgdtrasykqldgdtvtadtmlaaaigiqgmfatngrtvqveqdkiddkrslvsgni 1496
                                                                                                                                                                                                                                                                      1101 sddaggktggt-gatggtgg-----tgsggsattlstgdavrsttsgsgsgggsstgsgag 1154
                                                                                                                                                                               1377 slnsvlssldlalkgstvytlgvsstkskdgtyavifgyviasgytlvsprctlsiygst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 SADSGG--GGTPDATGGGGGGDTPSATGGGGGGDTPTATG-------GGGGG 165
                                               404 AMT 406
                                                                                                                                                                                                                                                                                                                                                                                                                271 ----ATLKNVNLGE------NEVDGI-----HVKAKNAQEVTIDNVH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 VSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGT---
                                                                                                                               VRTNGG-----KQFDD-------MSIELNGIEANHGKFALVKSDSDDLK--LATGNI 403
                                                                                                                                                                                                                                                                                                                      ---AQNVGEDLITVKGEGGAAVTNL-----NIKNSSAKGADD--KVVQLNANTH-----
                                                                                                                                                                                                                                                                                                                                                                rsslatvspisaaeqaiidaqkadvmnqlagimdgsasnnslntsssllnqisslpaadl 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gsdsngssgvstksssgsdt------sgssdssgangafsataqpstrttkt 1256
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Pred. No. 0.00029;
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RESULT 15

AAY95556 standard; Protein;

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Location of vulva; LOV-1 gene; nematode; mating behaviour; Caenorhabditis elegans LOV-1 (location of vulva) protein.

XEXEXXXX

10-OCT-2000

(first entry)

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Best Local S
Matches 96
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1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules from Caenorhabditis elegans useful for producing transgenic nematodes with altered mating behavior for identifying genes or regulatory factors involved in polycystic kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polycystin; polycystic kidney disease; animal model;
signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 114-123; 142pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                  271
                                                                                                                                                                                                                                                                                                                     125 SADSGG--GGTPDATGGGGGGDTPSATGGGGGDTPTATG-----
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 96; Conserv
                                  ---AQNVGEDLITVKGEGGAAVTNL-----NIKNSSAKGADD--KVVQLNANTH----- 346
                                                                                                                                                 gsdsngssgvstksssgsdt-----sgssdssgangafsataqpstrttkt 1256
                                                                                                                                                                                     VSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEG
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                                                                         rsslatvspisaaeqaiidaqkadvmnqlagimdgsasnnslntsssllnqisslpaadl 1316
                                                                                                                ----ATLKNVNLGE-----NEVDGI-----HVKAKNAQEVTIDNVH------
                                                                                                                                                                                                                                                               GGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3178 AA;
                                                                                                                                                                                                                                                                                                                                                                         8.1%; Score 177.5; DB 21; llarity 22.7%; Pred. No. 0.00033; Conservative 52; Mismatches 110;
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Search completed: October 4, 2001, 22:26:59 Job time: 2655 sec

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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
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Gapop 10.0 , Gapext 0.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/ABCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-460-746A-4
US-08-460-066-4
US-08-460-066-4
US-08-819-539-7
US-08-819-539-7
US-08-98-030-270A-7
US-08-98-020-770-761A-8
US-08-770-761A-7
US-08-710-761A-7
US-08-710-70-70-7
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	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
	146	146.5	147	148	149	. 149	149	149	149.5	149.5	150	150.5	150.5	150.5	150.5	150.5	150.5	151.5
	6.6	6.7	6.7	6.7	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9
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ALIGNMENTS	US-08-276-852-34	US-08-808-599A-24	US-08-496-944-2	US-09-060-756-728	PCT-US91-09133-27	US-08-923-854-26	US-08-463-667A-4	US-08-463-587A-26	US-09-206-537-8	US-08-845-998-8	US-08-387-942C-5	US-08-808-599A-3	US-08-728-626-3	US-08-738-975-3	US-08-751-965-3	US-08-439-818A-3	US-08-317-522A-3	US-09-402-668-10
	Sequence 34, Appl	Sequence 24, Appl	Sequence 2, Appli	Sequence 728, App	Sequence 27, Appl	Sequence 26, Appl	Sequence 4, Appli	Sequence 26, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 10, Appl					

## ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-120-817-2 RESULT 1 US-09-120-817-2 Sequence 2, Applic Patent No. 6172184 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/055,107 FILING DATE: 06-AUG-1997 ATTORNEY/AGENT INFORMATION: NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19603/1741 TELEPHONE: (716) 263-1304 TELEPHONE: (716) 263-1304 TELEFAX: (716) 263-160 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICANT: Charkowski, Amy APPLICANT: Alfano, James R. TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: APPLICANT: STRANDEDNESS: FILING DATE: CLASSIFICATION: ZIP: 14603 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester STATE: New York COUNTRY: APPLICATION NUMBER: US/09/120,817 LENGTH: amino acid Application US/09120817 424 amino acids U.S.A. Collmer, Alan 6) 263-1304 263-1600 2: Version #1.30

Query Match
Best Local Similarity
Matches 424; Conserv

Conservative

0;

100.0%;

Score 2200; DB 4; Pred. No. 1.7e-172; Mismatches

Length 424; Indels

0

Gaps

MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNEGTP

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SOFTWARE: PatentIn Vei
SEQ ID NO 2
LENGTH: 197
TYPE: PRT
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                                          Query Match
Best Local
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APPLICANT:
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                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: 9-24
PRIOR FILING DATE: 1997-09-08
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 1998-04-09
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR FILING DATE: 1997-04-09
                                                                                                                                                                                                                                                                                                                                     APPLICANT: TSUMADORI, Masaki
TITLE OF INVENTION: Detergent Composition
FILE REFERENCE: 2173-0116P
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                ORGANISM: Bacillus sp.
OTHER INFORMATION: Strain: KSM-P15
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226 VVKDTIKVGAGEVFDGHGATFTAD-KSMGNGDQGENQKPMFELAEGATLKNVNLGENEVD 284
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                            Local Similarity 40. hes 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTM 360
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SHIKATA, Shitsuw
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KOBAYASHI, Tohru
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                                                                                                                                                                                                                                                                                                                                                                                 Susumu
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                            14.5%; Score 318; DB 4 40.7%; Pred. No. 7e-19; tive 33; Mismatches
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                                                      DB 4; Length 197;
                            61;
                            Indels 14;
                           Gaps
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Sequence 1, Application US/09052995
Patent No. 6183956
GENERAL INFORMATION:
APPLICANT: Stvaraja, Mohanram
APPLICANT: Strulovici, Berta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 221
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Schnorr, Kirk
TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
FILE REFERENCE: 5377.200-US
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andersen, APPLICANT: Schulein,
                                                                                                                                                                              189 STSSVTMTNTRYSKVGQKWIGVKHATER 216
                                                                                                                                                                                                                    399 ATGNIAMTD------VKHAYDK 414
                                                                                                                                                                                                                                                                                                                                                                             279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                 VQLNANTHLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKL
                                                                                                                                                                                                                                                                                                                                                                                                                   EKALAAEVVHKTIVVEKGQTYDGKGKRLIAGPELGDGSQREDQKPIFKVEDGATLKNVVL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 221;
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APPLICANT:

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/09053003 Patent No. 6207391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wu, Per
APPLICANT: MCKinn
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
             SOFTWARE: Patentin Kel
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: High-Throughput Screening Assays for TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 GGLGTPSADSGGGGTPDATGGGGGDTPSATGGGGGGDTPTATGGGGSGGGTPTATGGGSG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GTPTATGGGEGG 190
                                                                                                                                  ZIP: 94111-3834
APPLICATION NUMBER:
                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39
                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Parent, Annette S. REGISTRATION NUMBER: 42,058 REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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California
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McKinney, Judi
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                                   PatentIn Release #1.0, Version #1.30
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us/09/053,003

 Mismatches

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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,987
FILING DATE: 03-SEP-1993
                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: Sim & McBurney
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
NAME: 35,367
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATLASHEWSKI, Gregory APPLICANT: CHAREST, Hugues
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                     STREET: Suite CITY: Toronto STATE: Ontario
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                                                     FILING DATE:
CLASSIFICATION: 424
                                                                                   APPLICATION NUMBER:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                         COUNTRY:
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les 36; Conserv
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amino acid
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                                                                                                                                                                                                                                                                           Suite 701,
                                                                                                                                                                                                                         Canada
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(415) 576-0300
(415) 576-0300
PR SEO ID NO: 40:
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                                                                                                                                                                                                                                                                       330 University Avenue
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/note= "Gly at positions 105-201 may
present or absent"
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                                                                                     US/08/452,531
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/note= "Gly at positions 1-97 may be
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Pred. No. 1.1e-06;
0; Mismatches 36
                                                                                                                       Version #1
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RESULT 7
US-08-460-746A-4
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Best Local Similarity
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                                     ATTORNEY/AGENT INFORMATION:

NUMBER: US 08/115,987
FILLING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GREENARM
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                  APPLICATION NUMBER: US 0: FILING DATE: 12-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       STREET: CITY: Toronto
CITY: Toronto
Ontario
Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHAREST, Hugues
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                              APPLICATION NUMBER: US/08/460,746A FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          COUNTRY: Canada ZIP: M5G 1R7
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                                   STEWART,
                                                                                                                                                                                                                                                                                                                                                                                                               6th Floor, 330 University Avenue
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FORma.
Michael 1.
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Pred. No. 1.7e-06;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115
PILING DATE: 03-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael 1.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MATLASHEWSKI, Gregory
APPLICANT: CHAREST, Hugues
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 PDSQAPFQNNG------GLGTPSAD----SGGGGT--PDATGGGGGDTPSATGGGGGDT 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 PKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSE-GPKGT 207
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                                                                                                                                                                     APPLICATION NUMBER: US 08/302,463 FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 PGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEGPKGTGGPGSEG 148
                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sim & McBurney
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                                                                                                                                                                                                                                                                                                                                                                                             TRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toronto
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                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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31.9%;
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                                                                                                              US 08/115,987
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1038-485 MIS:vg
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Pred. No. 1.7e-06;
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                                                                                                                                                                                                                                                                                                        Version #1.25
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US-08-460-066-4
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Best Local
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                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,463
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,987
FILING DATE: 03-SEP-1993
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-484 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                        NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Surronto
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TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED LEISHMANIA
TITLE OF INVENTION: GENES AND PROTEINS
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                                                                                                                                                                                                                                                        FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/460,066
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                 CLASSIFICATION:
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STRANDEDNESS: single
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31.9%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FRUGTH: 269 amino acids
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Best Local Similarity
Matches 58; Conserv
                                                                                  TELEFAX: (716) 263-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acid
                                                                                                                                        FILING DATE:
ATTORREY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 10-JUL-19
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
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STRANDEDNESS:
                                                                                                                       TELEPHONE:
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                 amino acid
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Linton Square, P.O. Box 1051
                                                                                                                           (716) 263-1
                                                                                                                                                                                                                                                                                                                                       10-JUL-1997
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                                                                                                      263-1600
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                                                                                                                                                                                                                                                                           08/475,775
                                                                                                                                                                                                                                                                                                                                                         US/08/891,254
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US-08-819-539-7
; Sequence 7, Application US/08819539
; Patent No. 5859324
; GENERAL INFORMATION:
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                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,539
FILING DATE: 17 MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wei, Zhong-Min APPLICANT: Beer, Steven V.
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 LGGGGAGAGGAGGAGGADGGSGAGGAGGANGADGGNGVNGNQANG-------
                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQILQQMLAAQNGGSQQST 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALLFGSDT-----QKD--VNFGTPD-----STVQNPQDASKP-NDSQSNIAKLISA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GGGGDTPSATGGGGGDTPTATGGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQITP 197
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                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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Pred. No. 6.6e-06;
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US-09-030-270A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09030270A Patent No. 5977060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
          FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,226
FILING DATE: 28-FEB-1997
FILING DATE: 28-FEB-1997
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wei, Zhong-Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 VQILQQMLAAQNGGSQQST 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                    STREET: P.O. Bo
CITY: Rochester
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                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 LIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGTPSADSGGGGTPDATG----- 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 344 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQA------IDP 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALLFGSDT-----QKD--VNFGTPD-----STVQNPQDASKP-NDSQSNIAKLISA 86
                                                                                                                                                                                                                                                                                                                                                                                                OF SEQUENCES:
                                                                                                                                                                                                                                                            14603
                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                      E: Nixon, Hargrave, Devans & Doyle LLP P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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INFORMATION
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HYPERSENSITIVE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 163.5; DB 2 23.2%; Pred. No. 6.6e-06;
                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                   US/09/030,270A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                      ELICITOR
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RESULT 13
US-08-984-207-7
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                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08984207 Patent No. 6235974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (716) 263-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      APPLICANT: Qiu, Dewen
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TRE
NUMBER OF SEQUENCES: 10
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acid
                                                                                                                                                                                             ADDRESSEE: Nixon, Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 19603/1521
TELECOMMUNICATION INFORMATION:
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                   JAKET: P.O. Box 1051, Clinton Square CITY: Rochester STAFE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 GAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKV------
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                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQILQQMLAAQNGGSQQST 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGTPSADSGGGGTPDATG----- 138
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                                                                                                         14603
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RATION NUMBER: 30,727
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                                                                                                                        U.S.A.
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16) 263-1600
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23.2%; Pred. No. 6.6
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               Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NLQSQIMDVV----KEV 320
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                                                                                                                                                                                                                                                    TREATMENT
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PCT-US96-08819-7
; Sequence 7, Application PC/TUS9608819
; GENERAL INFORMATION:
APPLICANT: COTHEL! Research Founds
TITLE OF INVENTION: RESISTANCE IN
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60 FILING DATE: 05-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Goldman, Michael L
                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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TOPOLOGY: 11
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                                           ZIP:
                                                       COUNTRY:
                                                                               STATE:
                                                                                                 CITY: Rochester
                                                                                                               STREET:
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                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1201
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                                                                           New York
                                                                                                                 E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                       COTTELL RESEARCH FOUNDATION, INC.
VENTION: HYPERSENSITIVE RESPONSE INDUCED
VENTION: RESISTANCE IN PLANTS
                                                         U.S.A.
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Pred. No. 6.6e-06;
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US-08-770-761A-8
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                                                                                                                                                                                                               Sequence 8, Application US/08770761A Patent No. 5814503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.4%; Score 163.5; DB 5
Best Local Similarity 23.2%; Pred. No. 6.6e-06;
Matches 88; Conservative 31; Mismatches 153
                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                  APPLICANT:
APPLICANT:
                                          APPLICANT: Otto, Keith A.

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS

NUMBER OF SEQUENCES: 8
                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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FILING DATE: 07-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                               321 VQILQQMLAAQNGGSQQST 339
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  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQA-----IDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q--NAGDVNGANGADD--GSEDQGGLTGVLQKLMKILNALVQMMQQGGLGGGNQAQGGSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-MQLLEDLVKL-LKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIEQILAQ 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSVG-----NIQSPSNLPGLQNLNLNTNTNSQQSGQSVQDLIKQVEKDILNIIAALVQK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GGGGDTPSATGGGGGDTPTATGGGSGGGGTPTATGGGSGGTPTATGGGEGGVTPQITP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman, Michael
                                                                                                                                                                  Kovacevic, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Eli Lilly and Company
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Search completed: October Job time: 3858 sec

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Best Local Similarity
Matches 99; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-DEC-199
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
459 ETIKDLMRQFLRGLD--FLHANCIVHRDLKPENILVTSGGTV
                                                                                400 EVALLRRLEAFEHPNVVRLMDVCATSRTDREIKVTLVF-EHVDQDLRTYLDKAPPPGLPA 458
                                                                                                                                                                                                       215 AGSTEQAGKINVVKDTIKVGA-GEVF---DGHGATFTADKS--MGNGDQGENQKPMFELA 268
                                                                                                                                                                                                                                                                                         155 TPTATGGGGSGGGTPTATGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVSDT 214
                                                                                                                                                                                                                                                                                                                                270 AAEEEEEEEE---EEVDLACTPTDVRDVDIASMGGG-----SGGGSG------GGSGG- 314
                                                                                                                                                                                                                                                                                                                                                                         102 QDTNQEQPDSQAPFQNNGGLGTPS-----ADSGGGGTPDATGGGGGGDTPSATGGGGGD 154
                                                                                                                                                                                                                                                                                                                                                                                                                   211 AVQG-LNLRSPNNFLSYYRLTRFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNMDPK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 TPHDFIEHFLSKMPE----AEEN-KQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Lilly Corporate Center/Patent Division CITY: Indianapolis
STATE: IN
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 TPLDF-SALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNF------GTPDS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                              -GGSMATSRYEPVAE-IGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGLPISTVR 399
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-447 <AUV
A;Cross-references: EMBL:Y13831; NID:e1293450; PID:e1293451; PIDN:CAA74158.1
A;Experimental source: strain CFBP1430; specific host Pommoideae
C;Genetics:

R;Gaudriault, S.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z18936
A;Accession: T18447

HrpW protein - Erwinia amylovora C;Species: Erwinia amylovora C;Species: Erwinia amylovora C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 C;Accession: T18447 R;Gaudriault, S. R;Gaudriault, S. Christoff Date Library Nov. 1998

RESULT T18447

## ALIGNMENTS

Best Local Similarity 36.1%; Pred. No. 1.7e-24; Best Local Similarity 47; Gaps  72 KPNDSQSNIAKLISALIMSLLOMLINSURGAGENDYNOMEGRAFONNGGIGGE
M M N M N M N M M M M M M

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C;Species: Bacillus Subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Caccession: A70045
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.Y; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Accession: A70045
A;Accession: A70045
                                                                                                                                                                                                             A;Title: Drosophila CBP is a co-activator of cubitus A;Reference number: Z17785; MUID:97263578 A;Accession: T13828 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             CREB-binding protein homolog - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000 C;Accession: T13828
     A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
C;Superfamily: bromodomain homology
F;1723-1780/Domain: bromodomain homolog
                                                                                                                         A;Molecule type: mRNA
A;Residues; 1-3190 <AKI>
A;Cross-references: EMBL:U88570; NID:g1916929; PID:g1916930;
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15500.1; PID:e1186183 A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 VVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 IHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDVKHA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLKIDNFKADDFGTMVRTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAM 405
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bromodomain homology
main: bromodomain homology <BRO>
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Pred. No. 7.3e-10;
2; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                          PIDN: AAB53050.1
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, (Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F5F19.6 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cross) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F96559
                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: F5F19.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-730 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005173; NID:g4220464; PIDN:AAD12691.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1467 --- AGGGSSTTPASNPLLLMSGGTAGGGTGATTTTSTSSSSRMMSSSSSSLSSQMAALEAA 1523
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                                                                                                                         127 APPPGSTGAK---
180 TNPGASA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 TPLDESALSGKSPQPNTFGEQN--TQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS 71
                                                            90
                                                                                                                                                                                                                                               Local Similarity
les 99; Conserv
                                                                                                                                                                            25 SPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGT---PDSTVQNPQDA--SKPNDSQSN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SADSGGGGTPDATGGGGGDTPSATGGGGG------DTPTA-----TGGGGSGGGGT 169
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                                                      IAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGT-PSADSGGGGTPDATG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAMDVDEAGGSTAGEH----HGEGGGGSGVGGGKDNINGAHDGGATGGAVDIKPKTETK 1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PQLANPNRTSGTGSVSDTAGSTEQAGKINVVK--DTIKVGAGEVFDGHGA 244
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   VGNGETEKNAGGSKPSS---
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                                                                                                                         -PGASGIGSDSGSIGSAGTNPGADGTRETEKNAGGSKPSSGSAG 179
                                                                                                                                                                                                                                            ; Score 215; DB 2;
; Pred. No. 5.8e-05;
46; Mismatches 180
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   -GSAGTNPGASAGGNGETEKNV 224
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Maiti, R.
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pectate lyase (EC 4.2.2.) C - fungus (Fusarium solani)
C; Species; Fusarium solani
C; Opate: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_cl
C; Accession: $68364
R; Guo, W.; Gonzalez-Candelas, L.; Kolattukudy, P.E.
Arch. Blochem. Biophys. 323, 352-360, 1995
A; Title: Cloning of a new pectate lyase gene pelC from Fusa
A; Reference number: $68364; MUID:96063610
A; Accession: $68364
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-219 <GUO>
A; Cross-references: EMBL:U13049
C; Genetics:
A; Gene: pelC
A; Introns: 52/1; 102/3
C; Keywords: carbon-oxygen lyase
probable myrosinase-binding protein - rape
N;Alternate names: jasmonate inducible protein
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1
C;Accession: 708080
R;Geshi, N.; Brandt, A.
Planta 204, 295-304, 1998
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                                                                                                                                             σ
                                                                                                                                                                                                                                                                                        AQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDEGTMVR 362
                                                                                                                                                                                                                                                                                                                                        Y--DRGSGACKGQNEGGDKDAVFLLHEGATLKNVIIGKDQSEGVHCKG----HCTLEFVW
                                                                                                                                                                                                                                                                                                                                                         FTADKSMG---NGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVH 302
                                                                                                                                                                                                                                                                                                                                                                                                             GYTGGV-PKPTDHISN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGEGGVTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGNGGNQWDD-GTDHDGVMKIH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMV 361
                                                                                                                                                                                               SCGNCSKQCKRNVYIEGVTAKNGG------ELAGINANYGDTATLKNVCADAK 196
                                                                                                                                                                                                                                                                   FEDVCEDAISIKED -- KAGKESWIIGGGAYHASDKVVQHNGCGTVNIINFYVEDYGKLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GASGIG-----NSDGSTGTSPEGTESNADGTKTNTGGKESNTGSESNTNSSPQKLEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNAGG-----SKSNDGANNGASGIESNAGSTGTNFGAGGTGGIGDTESDAGGSKTNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GGVTPQITPQLANPNRTSGTGSVSDTAGSTEQ---AGKINVVKDT-IKVGAGEVFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSKPSSGKAGTNPGANAGGNGGTEKNAGGSKSSSGSARTNPGASAGGNGETVSNIGDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GG------GGDTPSATGGGGGDTPTATGGGGSGGGG---TPTATGGGSGGTPTATGGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGGTNDGASGIGSNDGSTGTNPG---AGGGTDSNIEGTENNVGGKET---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.3%;
                                                                                                                                                                                                                              NGGKQFDDMSIELNGIEANHGKFALVKSDSDDLK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 205;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                     21-May-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VAVGGLGIEQIREDYVK
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.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                               ----SKVIEVKAGQVYDGKWAK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 219;
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                                                     11-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Y11483; NID:e1023101; PIDN:CAA72271.1; A;Experimental source: cv. Global; idolate a4; young seedlings A;Note: jasmonate inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Two jasmonate-inducible myrosinase-binding proteins A;Reference number: Z16340; MUID:98192006 A;Accession: T08080 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-680 <GES>
                                                                                               В
                                                                                                                                  Qγ
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                  F70806
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GGLGTPSADSGGGGTPDATGGGGGGDTPSATGGGGGGDTPTATGG------GGSGGGGTP 170
                                                                                                                                      376 --LNGIEA---
                                                                                                                                                                                                                                                        443 YEEFELASDEYITIVEGYYDKILGSDGLTSLTFHTNKGTYGPYGLEGSTHFEFKEDGHKI 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 KAGQPKQGALGGVQGSRGSTKEILINHPDEHLISVEGWYDSSNIIIGIQFKTNQKTSDYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 TGTGGTGTGGSGTGSGVEKLDAQGGTGGTAWDDGSDHDGVAKITVRTGGAGVQYVQFGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 -ANPNRTSGTGSVSDTAGSTEQA------GKINVV-----KDTIKVG--A
                                                                                             QTYDGIGAVKFVYNKGSSEIIGDEHGKSTLLGFEEFELNYPSEYI--TEVHGTYDKISAS
                                                                                                                                                                           TGFHGRAGATISAIGVYLAPVGTIPLTPATQTKKLEAKGGDGGTTWDDGAFDGIRKVSVG
                                                                                                                                                                                                                                                                                                                                      GGESGAVWDDGAHDNVKKVSVGQ-----GTDGIAAVKFEYRNGSSVVIGAERGTPTLLG
                                                                                                                                                                                                                                                                                                                                                                          NAQEVTI-----DNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSA----
                                                                                                                                                                                                                                                                                                                                                                                                                 GYDFDGSGTKFTL-QVQGKKIIGFHGFRQRPSQFNWERISVPVSTSTDPSTVPPKKLEAK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEVFDGHGATFTADKSMGN---GDQGENQKP-MFELAEGATLKNVNLGENEVDGTHVKAK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGG-GSGGTPTATG-----GGEGGV-----TPQITPQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%;
                                                                                                                                                                                                                                                                                             -KGADDKVV--
                                                                                                                                                                                                                 ---GTMVRT------NGGKQFDDMSIE-----
                                                                                                                                    --- NHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 204.5; DB 2;
Pred. No. 0.00021;
3; Mismatches 139;
                                                                                                                                                                                                                                                                                               ---QLNANTH--LKIDNFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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H37RV)
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A; Molecule type: DNA
A; Residues: 1-1901 <COL>
A; Cross-references: GB; AL022022; GB; AL123456;
A; Cross-references: Strain H37Rv A; Experimental source: strain C; Genetics: A; Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; A; Title: Deciphering the biology of Mycobacterium A; Reference number: A70500; MUID:98295987 A; Accession: F70806 A; Gene: Rv3508 C; Superfamily: A;Status: preliminary; nucleic acid sequence collagen alpha 1(IV) chain not shown; translation NID:g3261554; Whitehead, S.; Barrell tuberculosis from the PIDN:CAA17745.1; PID:g292 Barrell, B.G. not complete Holroyd, geno

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hypothetical protein R08B4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24045 R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obic membrane-anchoring sequence.
c;Comment: There are 17 tandem copies of the 11-residue repeat
C;Superfamily: circumsporozoite protein; thrombospondin type 1
C;Keywords: sporozoite; surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-401 <GAL>
C; Comment: There are three distinct regions in the mature circumsporozoite protein,
                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;20-401/Product: circumsporozoite protein #status predicted <
F;98-278/Region: 11-residue repeats
F;326-379/Domain: thrombospondin type 1 repeat homology <THRl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 48, 311-319, 1987
A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878
A;Accession: E26255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: E26255
R;Galinski, M.R.; Arnot, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circumsporozoite protein precursor - Plasmodium cynomolgi (strain
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Matches
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                         281
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                                                                                                                                                                                                                                                                                                                                                                                                119 GGLGTPSADSGGGGTPD---ATGGGGGGDTPSATGGGGGDTPTATGGGG-----SGGGGT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                              KDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGAGGAGD------NNFNGGQGGAGGQGGQGGLGGASTTSINANGG
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                                                                                                                                                                                                                                                                                                                 PTATGGGSGGT - - PTATGGGEGGVTPQ1TPQLANPNRTSGTGSVSDTAGSTEQAGKINVV
                                                                                                                                                                                                                                                                                                                                                        GGGGNDGAAAAGGGGNDGAAAAGGGGNDGAAAAGGGGNDGAAAAGGGGNDGAAAAGGGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GDGAT-GAAGLGDNGGYGGDGGAGGAAG-----NGGNAGYGLTAKAGDGGAAGNGGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                       -RAGDQQPPAGGNKKAGEAGGNAGAGQGQN----NEGANVPNAKLVKEYLDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.0%;
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3; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 197.5; DB 1
Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 401;
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hypothetical protein slr1403 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S77300

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; P.

C, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
S77300
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A;Map position: X
A;Introns: 53/2; 113/1; 152/3; 204/3;
멍
                                 δÃ
                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-3016 <KAN>
A; Residues: 1-3016 <KAN>
A; Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAA17634.1;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                              A; Reference number: S74322; MUID:97061201
A; Accession: S77300
A; Status: nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1226 <WIL>
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                                                                             Local Similarity
les 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 QNTQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS-KPNDSQSNIAKLISALIMSLL 92
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                                   22 SGKSPQPNTFGEQNTQQAIDPSALLFGS------DTQKDVN-----FGTPDSTVQ 65
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  AGANASPDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QGYNALTYQSSSKPPPPSDFIDIPNDPTLGGPTGSSGGGGGGGGGGGGGGGGGGGGGGG
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26.98;
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20.9%; Pred. No. 0.0046;
tive 63; Mismatches 180
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Pred. No. 0.
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da, м.; Yas
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NPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQA----

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A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status pred:
F;1-1106/Product: female sterile homeotic protein, 110K #status pred:
F;59-116/Domain: bromodomain homology <BRO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             k; Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, 1 Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect A;Reference number: A43742; MUID:89276730
A;Accession: A43742
                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1106 <HA2>
                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-2038 <HAY>
A; Cross-references: EMBL:M23221; NID:g157452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
C;Accession: A43742; B43742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster) N;Alternate names: membrane protein fsh, 205K N;Contains: female sterile homeotic protein, 110K
                                                                                                                                                                                                                                                                A;Cross-references: EMBL:M23222
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFDGHGATFTADKSMGNG-DQGENQKPMFELAEGATLKNVNL------GENEVDGI-
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Conservative
                                                                                                  bromodomain
                  8.8%;
                                                                                                homology
40;
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                  Score 193; DB 2;
Pred. No. 0.0033;
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Mismatches
                                                                                                  <BR02>
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  133;
                                   Length 2038;
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Indels
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                                                                                                                                          <MAT>
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14;
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RNA-binding protess. RNA-binding protess. RNA-binding protess. RNA-binding protess. RNA-binding protess. RNA-binding procession: Sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S33799; S36157 C;Accession: S33799; S36157 RNA-binding procession: Sapiens RNA-binding RNA-binding Procession: Sapiens RNA-binding RNA-bindin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: liposarcoma R;Rabbitts, T.H.; Forster, A.; Larson, R.; Nathan, P. Nature Genet. 4, 175-180, 1993
Nature Genet. 4, 175-180, 1993
A;Title: Fusion of the dominant negative transcription regulator CHOP with A;Reference number: S36157; MUID:93350637
A;Accession: S36157
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: RNA binding; probable plays a role in transcriptional regulation C;Superfamily: RNA-binding protein EWS; ribonucleoprotein repeat homology C;Keywords: carcinogenesis; nucleus; RNA binding; tandem repeat
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A; Residues: 1-63'S', 66-526 <RAB>
A; Cross-references: EMBL:X71428; NID:g393415; PIDN:CAA50559.1; PID:g4210363
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A;Map position: 16p11.2-16p11.2
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A; Residues: 1-526 < CRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;286-361/Domain: ribonucleoprotein repeat homology
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Best Local
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   86
                                                                          52 QKDVNFGTPDSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQP--
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SSQSSYG--
                                                                                                                                                                                                                   QQTTTPLDFSALSGKSPQPNT-----
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                                                                                                                                            QQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYG-STGGYGSSQ 85
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96; Conserv
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                                                                                                                                                                                                                                                                                         Conservative
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   -QQSSYPGYGQQPAPSSTSGSYGSSSQSSSYGQPQSGSYSQQPSY
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                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                          Score 191.5; DB 1
Pred. No. 0.00082;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                               -----FGEQNTQQAIDPSALLFGSDT 51
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hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37 C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: D70807 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
RESULT
G02127
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C;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1489 <COL>
A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17751.1; PID:g29244:
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                       KINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENE
                                                                                                                                                                                                                                             AGGSGGSSCAGGTNGSGGAGGTCGQVVAGGAGISFSNGSNGGTGGTGGVGGTGGDGGNAG
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                                                                                                                                                                                                                                                                                      -GGSGGTPTATG----GGEGGVTPQITP-----QLANPNR--TSGTGSVSDTAGSTEQAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 189.5; DB 2;
Pred. No. 0.0036;
2; Mismatches 74;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: A70893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fus-like protein - human (fragment)
(;Species: Homo sapiens (man)
(;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
(;Accession: G02127
R;Itoh, K.; Kawase, M.
submitted to the EMBL Data Library, September 1995
A;Reference number: G09199
A;Accession: G02127
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
A70893
APORSOS
C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999
C;Accession: A70893
A;Gene: Rv1067c
C;Superfamily: unassigned collagens
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                                                                          A; Experimental
                                                                                                                          A; Molecule type: DNA
A; Residues: 1-667 <COL>
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                                                                                                      A; Cross-references:
                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GGGR--GGRGGMGGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGEN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSGSGGGGSYGQDQSSMSGSGGGGG------GGGGG-----GSGGGGGYGNQDQSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSTDTGYGQSSYSSYGQSQNTGYGTQSAPQGYG-STGGYGSSQSSYGQQSS---YPG
                                                                            ices: GB:AL021897; GB:AL123456; NID:g3256022;
source: strain H37Rv
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                                                                                                        PIDN:CAA17183.1;
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Holroyd,
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Search completed: October 4, 2001, 22:27:53 Job time: 234 sec
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                                                                      340 QLNANT 345
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659 FGNAGT 664
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Result
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FUS_BOVIN
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MEDLINE-89276730; PubMed-2567251;

MEDLINE-89276730; PubMed-2567251;

Haynes S.R., Mozer B.A., Bhatla-Dey N., Dawid I.B.;

"The Drosophila fsh locus, a maternal effect homeotic ge apparent membrane proteins.";

Dev. Biol. 134:246-257(1989);

Dev. Biol. 134:246-257(1989);

The FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION
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Pterygota; Neoptera; Endopterygota; Diptera; Brachyo
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                                                                                                                                                                                                                                                                                                   "The circumsporozoite gene of the Plasmodium cynomolgi complex."; Cell 48:311-319(1987).
-!- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMI
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-OCT-2000 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
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Nussenzweig R.S., Enea V.;
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Eukaryota; Alveolata; Apicomplexa; H
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                                                                                                                                   MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEWOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                              MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
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01-JUN-1994
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SEQUENCE FROM N.A. (LONG 150000)
MEDLINE-93288139; PubMed-8510758;
Aman P., Mandahl N., Ron
                                                                                         Crozat A., Aman P., "Fusion of CHOP to a liposarcoma.":
                    SEQUENCE FROM N.A. (SHORT ISOFORM).
MEDLINE-93350637; PubMed-7503811;
Rabbitts T.H., Forster A., Larson R.,
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003067; -.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
PROTEIN FUS (ONCOGENE FUS) (ONCOGENE TLS) (TRANSLOCATED PROTEIN) (POMP75) (75 KDA DNA-PAIRING PROTEIN).
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Forster A., Larson R., Nathan P.; dominant negative transcription regulator CHOP with by translocation t(12;16) in malignant liposarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā,
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                 P., Mandahl N., Ron D.;
to a novel RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KKDEKQVEP--KKPRENKLKQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGD--
                                                                                                                                                                                                                                                                                                                                                                                                            -AGGNKKAGEAGGNAGAG---QAQNNEAANVPN--AKLVKE
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Pred.
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17 X 11 AA TANDEM REPEATS
A-A-G-G-G-G-N.
; 57D666268238503E CRC64;
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                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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No. 0.0018;
smatches 121;
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                                                                                                 myxoid
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EMBL; S62140; AAB27102.1; -.
EMBL; S62138; AAB27103.1; ALT_SEQ.
EMBL; X71427; CAA50558 1; ALT_SEQ.
EMBL; X71428; CAA50559.1; ALT_SEQ.
EMBL; X71428; CAA50559.1; ALT_SEQ.
EMBL; AF071213; AAC35285.1; -.
EMBL; AF071213; AAC35284.1; -.
PIR; S33799; S33799.
HSSP; P09651; 1HA1.
                      MIN; 13.300; IPR000504; -.
Interpro; IPR000504; -.
Interpro; IPR001876; -.
Pfam; PP00076; rrm; 1.
Pfam; PF000641; zf-RanBP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99369251; PubMed=10442642;
Bertrand P., Akhmedov A.T., Delacot
"Human POMp75 is identified as the
POMp75 and POMp100 DNA homologous p
to cell prolifieration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20036580; PubMed=10567410; Baechtold H., Kuroda M., Sok J., Ron D., Lopez B.S., "Human 75-kDa DNA-pairing protein is identical to th TLS/FUS and is able to promote D-loop formation."; J. Biol. Chem. 274:34337-34342(1999).
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94243799; PubMed-8187069;
Ichikawa H., Shimizu K., Hayashi Y., Ohki M.;
"An RNA-binding protein gene, TLS/FUS, is fused to ERG in
myeloid leukemia with t(16;21) chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Res. 54:2865-2868(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 18:4515-4521(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 265-276; 317-331 AND 335-357,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 221:191-198(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morohoshi F., Ootsuka Y., Arai I
Munakata N., Ohki M.;
"Genomic structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
MEDLINE-99013873; PubMed-9795213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOMAL TRANSLOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 235-244; 307-312;
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEI
SIMILARITY: CONTAINS 1 RANBP-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND CHOP.
DISEASE: A FORM OF ACUTE MYELOID LEUKEMIA (AML) :
BY A CHROMOSOMAL TRANSLOCATION T(16:21)(P11:Q22)
FUS AND ERG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: UBIQUITOUS.

DISEASE: A FORM OF MALIGNANT MYXOID LIPOSARCOMA
BY A CHROMOSOMAL TRANSLOCATION T(12;16)(Q13;P11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-
STRANDED DNAS AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED
DNA, MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY.
SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)
AND A SHORT ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                    137070; -.
151900; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet. 4:175-180(1993).
PS50102; RRM; 1.
PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ootsuka Y., Arai K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TET FAMILY OF RNP PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RBP56/hTAFII68
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                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durrbach
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) THAT INVOLVES FO
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K1CI_HUMAN STANDARD;
P35527; Q14665;
Ol-JUN-1994 (Rel. 29, Created)
Ol-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
KERATIN, TYPE I CYTOSKELETAL 9 (CYTOKERATIN 9)
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CONFLICT
SEQUENCE
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ZN_FING
                                                                   TISSUE-FOOT SOLE TISSUE; TISSUE-FOOT SOLE TISSUE; PROOF SOLE TISSUE; PROOF SOLE TISSUE; PAURILINE-94/13/1202; PubMed=7507869; Langbein L., Heid H.W., Moll I., Franke W.W.; Molecular characterization of the body site-specific cytokeratin 9: cDNA cloning, mano acid sequence, and specificity of gene_expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proto-oncogene; RNA-binding; DNA-binding; Nuclear protein; Repeat; Alternative splicing; Chromosomal translocation; Zinc-finger; Zinc
   MEDLINE=90267446;
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                     SEQUENCE OF 449-465
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   PubMed=2140676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GGGR--GGRGGMGGSDRGGFNKFGGPRDQGSRHDSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 191.5; DB 1; Pred. No. 0.0027;
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TG -> S (IN SHORT ISOFORM).
T -> N (IN REF. 4).
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BREAKPOINT FOR TRANSLOCATION
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ARG/GLY-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359
                                                                                                                                                                                                                                 Hominidae;
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                                                                                         human epidermal
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                                                                                                                                                                                                                                                                                                                                                      MATURE PALMAR AND PLANTAR SKIN TISSUE OR IN THE MORPHOGENIC PROGRAM OF THE FORMATION OF THESE TISSUE.

-I- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
-I- TISSUE SPECIFICITY: EXPRESSED IN THE TERMINALLY DIFFERENTIATED EPIDERMIS OF PALMS AND SOLES.
-I- DISBASE: DEFECTS IN KRT9 ARE A CAUSE OF EPIDERMOLYTIC PALMOPLANTAR KERATODERMA (EPPK), AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY DIFFUSE THICKENING OF THE EPIDERMIS ON THE ENTIRE SURFACE OF PALMS AND SOLES SHARPLY BORDERED WITH ERYTHEMATOUS MARGINS.
-I- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 KDA) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K8].
-I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILLAMENT FAMILY.
-I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILLAMENT FAMILY.
-I- CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE A 60 KDA CHAIN OF PLACENTAL SCATTER PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothnagel J.A., Wojcik S., Liefer K.M., Dominey A.M., Huber Hohl D., Roop D.R.;
"Mutations in the 1A domain of keratin 9 in patients with epidermolytic palmoplantar keratoderma.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen E.M., Meromsky L., Romero R., Setter E., Goldberg I "Human placenta contains an epithelial scatter protein."; Biochem. Biophys. Res. Commun. 168:1082-1088(1990).
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Dreschler M., Schroek E., Royer-Pokora B., Franke W.W., (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).";
                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                      (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                ntermediate filament;
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461
152
188
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N -> K (IN EPPK).

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R -> Q (IN EPPK).

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R -> W (IN EPPK).
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LINKER 1.
COIL 1B.
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SEQUENCE FROM N.A.
MEDLINE=93054906; PubMed=1385442;
Wente S.R., Rout M.P., Blobel G.;
"A new family of yeast nuclear pore complex proteins.";
J. Cell Biol. 119:705-723(1992).
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SEQUENCE
                              Submitted -!- FUNCTI
                                                                                                          SEQUENCE FROM N.A. MEDILINE=9309980; PubMed=1464327; MEDILINE=509980; PubMed=1464327; Mehrba Wimmer C., Doye V., Grandi P., Nehrba "A new subclass of nucleoporins that nuclear pore protein NSP1."; EMBO J. 11:5051-5061(1992).
                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-FBE 1996 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NUCLEOPORIN NUP116/NSP116 (NUCLEAR PORE PROTEIN NUP116/NSP116).
NUP116 OR VMR047C OR VM953.12C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                               Q02630;
01-JUL-1993
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                                                         Odell C.,
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NCBI_TaxID=4932;
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Ill C., Bowman S., Barrell B.G., Rajandream M.A.;
mitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
miction: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION
THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
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EMBL; Z48502; CAA88413.1; -.
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-!- SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                              110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2329;
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for
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                                                                                                                                                                                                                                     င်
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                                          EMBL; M34398; AAA3944
EMBL; U09189; AAA8215:
PIR; A35628; A35628.
HSSP; P10968; 1WGC.
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01-NOV-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mehrel T., Hohl D., Rothnagel J.A., Longley M.A., Bundman D., Cheng C., Lichti U., Bisher M.E., Steven A.C., Steinart P.M., Yuspa S.H., Roop D.R.;
"Identification of a major keratinocyte cell envelope protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LORI_MOUSE P18165;
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                              "The proximal promoter of the mouse loricrin gene contains a functional AP-1 element and directs keratinocyte-specific but no differentiation-specific expression.";
J. Biol. Chem. 270:10792-10799(1995).
-i- FUNCTION: MAJOR KERATINOCYTE CELL ENVELOPE PROTEIN.
-i- SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND N-(GAMMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 61:1103-1112(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Roop D.R.
                                                                                                                                                                                                                                                                                                                                                    DiSepio D., Jones A., Longley M.A., Bundman D., Rothnagel J.A.,
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95256248; PubMed=7738016;
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB,
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90275605; PubMed=2190691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
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                           MGI:96816; Lor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYLTGDTRASYKQLDGDTVTADTMLAAAIGIQGMFATNGRTVQVEQDKIDDKRSLVSGNI
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   481 AA;
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(Rel.
(Rel.
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letazoa; Chordata;
ltheria; Rodentia;
                                                                     AAA39444.1;
AAA82152.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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35,
   37830
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Last annotation updat
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   WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
   97349A786FF239FE CRC64;
                                                                                                                                                                                                                                                                                                           keratinocyte-specific but not
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There are no restrictions on ong as its content is in no
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Query Match

7.88;

Score 172.5;

DB 1;

Length 481;

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THE RESULT TO SOLVE THE RE
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Best Local
                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S_MOUSE
FUS_MOUSE
P56959;
01-OCT-2000
01-OCT-2000
                                                                                                                                                DOMAIN
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                     Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alappat S.R., Zhang
Burdsal C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    RNA-binding;
                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
SGKSPQPNTFGEQNT-----QQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDASKPND 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGGGSSCGGGGGYSGGGGTSCGGGSSGGGGGGSSQQ
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                                                                                                                                                                                                                                                                                                                                                                                   AF224264; AAF70602.1;
                                         84;
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                                                                   PS50102; RRM; 1.
PS00030; RRM_RNP_1;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                               DNA-binding;
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Rođentia;
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                                                                                                                                                   52673
                                                               7.8%;
23.7%;
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                                                                                                                                                   WW;
                                         45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is not removed.
                                                               Pred.
                                                               Score 172.5; DB Pred. No. 0.024;
                                                                                                                                                                    ARG/GLY-RICH.
C4-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                     FALSE_NEG.
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                                                                                                                                                                                                                               GLN/GLY/SER/TYR-RICH GLY-RICH.
                                                                                                                                                                                                          RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alliegro M.A.,
                                                                                                                                                                                                                                                                                             protein; Repeat;
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                                                                               DB 1;
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                                       122;
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                                         Indels 103;
                                                                                 Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.C.,
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Y747_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JU-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV0747 PRECURSOR.
RV0747 OR MTV041.21.
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053810;
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                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston Taylor K., Whitehead S., Barrell B.G.,
                                                Hypothetical protein; Repeat; SIGNAL 1 30
                                                                                   Pfam; PF00934; PE;
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EMBL; K00772; AAA29556.1; -.
PIR; A03389; OZZQAK.
InterPro; IPR000884; -.
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"Identification and Chemical synthesis of a tandemly repeated
immunogenic region of Plasmodium knowlesi circumsporozoite protei
Nature 305:29-33(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the plasmodium knowlesi circumsporozoite protein."; cell 34:815-822(1983).
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PRINTS; PR01303; CRCMSPRZOITE.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV1983.
RV1983 OR MTCY39.36C.
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01-NOV-1997
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30-MAY-2000
                    MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV
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Pfam; PF00934; PE; 1.

Hypothetical protein; Transmembrane.
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TRANSMEM 332 352 POTENTI
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TubercuList; Rv1983;
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POTENTIAL.
POTENTIAL.
17ECBE43778E021E (
  Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VTEPTVHANVNGGPTSTILVDTGSAGLVVSPEDV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 170;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                on update)
                                                                                                                                                                                                                                                                                                                                                 Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
  tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363
                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
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  the
                                                                                                                                                                                                Harris
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                        Drosophila
Eukaryota;
Pterygota;
                                                                                                                                                                                                                                             MAM_DROME
P21519;
01-MAY-1991
01-MAY-1991
01-MAR-1992
         unusually rich in amino acid homopol Genes Dev. 4:1688-1700(1990).
-!- FUNCTION: MAY HAVE A REGULATORY
                                    "The Drosophila neurogenic locus unusually rich in amino acid home
                                                                            MEDLINE=91065516; PubMed=1701150; Smoller D., Friedel C., Schmid A.
                                                                                                                                                                                                                     MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                  Yedvobnick B
                                                                                                          STRAIN=CANTON-S;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NEUROGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
Nature 393:537-544(1998).
-i- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z80225; CAB02341.1;
HSSP; P04002; LATF.
TubercuList; Rv2634c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 778 AA; 63131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00934; PE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000084; InterPro; IPR001899;
                                                                                                                                                                                                                                                                                                                                                                       494
                                                                                                                                                                                                                                                                                                                                                                                                  316
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                                                                                                                                                                                                                                                                                                                                                                       AGGKGGQGHNTGVGDAFGGD
                                                                                                                                                                                                                                                                                                                                                                                                EGGAAVTNLNIKNSSAKGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLGTPSADSGGGGTPDATGGGGG - DTPSATGGGGGDTPTATGGGGGSGGGTPTATG - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLIT-----VKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt GGDGAPGGDGGAGPLLIGNGGVGGLGGAGAAGGNGGAGGMLLGDGGAGGQGGPAVAGVLG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGGPGPAGGVGEAGGVGG-----QGGLGESLDGNDGTGGKGGAGGTAGTDGGAGGAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 29.76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGSGGTPTATG----GGEGGV----TPQITP-QLANPNR----TSGTGSVSDT--
                                                                                                                                                                        Metazoa; Arthropoda;
Neoptera; Endopterygo
                                                                                                                                                            melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musca; Drosophildae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGSTEQAGKINVVKDTIKVGAGEVFDGH-----
                                                                                                                                                                                                                                             (Rel. 18, Created)
(Rel. 18, Last sequence up)
(Rel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                           GAG-----GIGETDG-
                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                  MASTERMIND
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29.2%;
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Pred. No. 0.048;
                                       homopolymers
                                                                             Α.,
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                                       mastermind
opolymers.";
                                                                             Bettler D.,
            FUNCTION
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                                                                                                                                                                                                                                                                                                    1596
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                                                                                                                                                                                                                                                                                                                                                                                                                             -SAGGVATGGEGGDGATGGVDGGVGG
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              ASSOCIATION
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                                                  protein
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Query Match
Best Local
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DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PIR; A36391; A36391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase;
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534
                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                     188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THE PROTEIN HAS MANY AA HOMOPOLYMERIC DOMAINS: POLY-GLN RUNS (FROM 5 TO 16 AA IN LENGTH), 4 POLY-GLY (6 TO 10 AA), 3 POLY-ASN (3 X 5 AA), 1 POLY-ALA (10 AA) AND 1 POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: DURING EARLY NEUROGENESIS UBIQUITOUSLY LOCATED. DURING LATER STAGES THEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR.
                                                              DGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGG 318
                                                                                                                                                                                           DGHGATFTADKSMGNGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGGGGSG-----PTATGGGSGGTPTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVTVKALTN-----TSVKSEPGVG------GGGG-----GGGGGNSGNNNNNNGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSNTGNNTN-NNGNSTNNN---GGSNNNGSENLTKFSVEIVQQLEFTTSPANSQPQQIST 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSDTQKDVNFGTPDSTVQNPQDASKPNDSQSNIAKLISALIMSL------LQMLT 96
DGIKVEPPNAQDLI --
                                                                                                                                                                                                                                                       AGGLGGMGMPPNMMSAQQKSALGNLANLVECKREPDHDFPDLGSLD-----KDGGGGQF
                                                                                                                                                                                                                                                                                                                     EGGVTPQ-ITPQLANPNRTSGTGSVSDTAGSTEQ------AGKINVVKDTIKVGAGEVF 239
                                                                                                                                                                                                                                                                                                                                                                                    ---GGGGNGNNNNNGGDHHQQQQQHQHQQQQQQQQGGGLGGLGNNGRGGGPGGMATGPGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSNKKQDTNQEQPDSQAPFQNNGGLGTPSADSGGGGTPDATGGGGGDTPSATGGGGGDTP 156
                                                                                                                             PGFPDLLGDDNSENNDTFKDLINNLQDFNPSFLDGFDEKPLLDI--
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190
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1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 170; DB 1; Length 1596; 22.7%; Pred. No. 0.1;
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GLY/ASN-RICH.
GLY-RICH.
GLY-RICH.
GLN-RICH.
GL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASP/GLU-RICH (ACIDIC).
W; B944D86EF359D605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH (BASIC).
                                                                                                                                                                                        -----QGENQKPMFELAEGATLKNVNLGENEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat.
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30-MAY-2000 (Rel. 39, Last sequence update)

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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MCBI_TaxID=1773;
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FLIGSGGTGGVGGAATTTGGVGGAGG----NAGLLIGAAGLGGCGGGAFTAGVTTG
                                                    QLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMG 253
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Query Match 100.0%; Score 2200; DB 2; Best Local Similarity 100.0%; Pred. No. 1.5e-128; Matches 424; Conservative 0; Mismatches 0;

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J. Bacteriol. 180:5211-5217(1998).

EMBL; AF037983; AAC62530.1;
-SEQUENCE 441 AA; 44714 MW; 7B3B3146E51897BB CRC64;
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Comparison of the hrpN-flanking regions of two Erwinia strains with different host specificity.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083620; AAF63402.1;
SEQUENCE 447 AA; 45340 MW; OBBAEA3871EDC2F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia amylovora
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           FTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMTDVKHAYDKTKASTQHTEL
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FTAGSELGDGGQSENQKPLFILEDGASLKNVTMGDDGADGIHLYG----DAKIDNLHVTN
                                            {\tt SPTKAAGGSTPVTDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVKASQVFDGKGQT}
                                                                                          GTGNSSASSGTSSSGGSPFNDLSGGKAPSGNSPSGSYSPVSTFSPPSTPTSPTSPLDFPS
                                                                                                       GGDTPTATGGGGSGGGTPTATGGG----SGGTPTATGGGEGGVTPQITPQL-------A
                                                                                                                                         TTPQSDSQNMLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMMDGQSDQFGQP
                                                                                                                                                                  -TPSADS----
                                                                                                                                                                                       QPIDRQTIEQMAQLLAELLKSL---LSPQSGNAATGAGGNDQTTGVGNAGGLNGRKGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMTDVKHAYDKTQASTQHTEL
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                                                                                                                                                                                                                                     147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
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O (TrEMBLrel. 15,
O (TrEMBLrel. 15,
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36.1%;
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                                                                    -TGSVSDTAGS----TEQAGKINVVKDTIKVGAGEVFDGHGAT
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Last sequence update)
Last annotation update)
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Pred. No. 1.9e-27;
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VGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNANTHLKIDNFKADDFGTMVRTNG

VGEDAITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVRTNG

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Matches 147
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054508;
01-JUN-1998
                                                                                                            homologous to pectate lyases of a distinct class.";
J. Bacteriol. 180:5203-5210(1998).
EMBL; V13831; CAR74158 1; -.
EMBL; U97504; AACCACC.
                                                                                                                                                                                                                                STRAIN=EA321, ATCC 49947;
Kim J.F., Zumoff C.H., Beer S.V
"HrpW, a new harpin of Erwinia
pectate lyases.";
                                                                                                                                                                                                                                                                                               Bogdanove A.J., Kim J.F., Wei Z., Kolchinsky P., Char Conlin A.K., Collmer A., Beer S.V.; Conlin A.K., Collmer A., Beer S.V.; "Homology and functional similarity of an hrp-linked locus, dspEF, of Erwinia amylovora and the avirulence Pseudomonas syringae pathovar tomato."; Proc. Natl. Acad. Sci. U.S.A. 95:1325-1330(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaudriault S., Malandrin L., Paulin J.P., Barny M.A.; "DspA, an essential pathogenicity factor of Erwinia amyl homology with AvrE of Pseudomonas syringae, is secreted secretion pathway in a DspB-dependent way."; mol. Microbiol. 26:1057-1069(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRPW.
                                                                                                 EMBL; U97504; AAC04849.1; EMBL; U94513; AAC62314.1;
                                                                                                                                                                           STRAIN=EA321, ATCC 49947;
MEDLINE=98422475; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwinia amylovora.
Bacteria; Proteobacteria;
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                                                                                                                                                                    Kim J.F
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CFBP1430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98086111; PubMed=9426142;
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GKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAY
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                                Score 559; DB
Pred. No. 3.4e
54; Mismatches
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                                  Indels
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Best Local (
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                                                                                                                                                                                                                                                    Lyase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1409;
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01-MAY-2000
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                                                                                                          285 GIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAVTNLNIKNSSAKGADDKVVQLNAN
                                                                                                                                                       226 VVKDTIKVGAGEVFDGHGATFTAD-KSMGNGDQGENQKPMFELAEGATLKNVNLGENEVD
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                                              GTINIRNFRADDIGKLVRQNGGTTY-KVVMNVENCNISRVKDAILRTDS---STSTGRIV
                                                                                            GVHCYG----DCTITNVIWEDVGEDALTLKSSG----
                                                                                                                                            VVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVIGAPAAD
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40.7%;
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Pred. No. 1.1e
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01-JAN-1998
01-JAN-1998
01-NOV-1998
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Q9x6z2;
01-NOV-1999
MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Rzevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                          YVPA.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Submitted (APR-1999) to the
EMBL; AJ37980; CAB40884.1;
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SIGNAL
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                                                                                                                          Karamata
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                                                                                                                                    Lazarevic V.,
                                                                                         EQUENCE FROM N.A.
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Pred. No. 1.7e
33; Mismatches
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EMBL/GenBank/DDBJ
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RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harawood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rasto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sckiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Wassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Vasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus
subtills.";
""Subtills.";
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Best Local s
Matches 68
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                                     SEQUENCE FROM STRAIN=A3(2);
                                                                                                                                                                                                                                         Streptomyces coelicolor. Bacteria; Firmicutes; Ac
Saunders D.C.,
                                                                                                                                                          NCBI_TaxID=1902;
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Pred. No. 4.9e
32; Mismatches
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R InterPro; IPR0001487; ...

InterPro; IPR001487; ...

InterPro; IPR003101; ...

Pfam; PF00439; brown ...

Pfam; PF00467; pffam; PF00867; ...
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CREB-BINDING PROTEIN HOMOLOG.
NEJ OR CG15319.
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001368;
01-JUL-1997
01-JUL-1997
01-MAR-2001
                                                                                            signalling.";
Nature 386:735-738(1997).
EMBL; U88570; AAB53050.1;
HSSP; P03622; 2IFO.
                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97263578; PubMed-9109493;
MEDLINE-97263578; PubMed-9109493;
Akimaru H., Chen Y., Dai P., Hou D.X., Nonaka
Armstrong S., Goodman R.H., Ishii S.;
"Drosophila CBP is a co-activator of cubitus i
                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trachbatta; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL: AL445503; CAC13062.1; -.
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Cerdeno A.M., Parkhill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPMFELAEGATLKNVNLGENEVDGIHVKAKNAQEVTIDNVHAQNVGEDLITVKGEGGAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNGSEGVSSTLSVSGTKDYGMK-----RLYGTGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGATFTADKSMGNGDQGENQ
                                                                                                                                                                                                                                                                                                                                                                                                          EVNWKGGRIAGINTNYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                EAN--HGKFALVKSDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       --YTVSGGGAKEADDKVFQFNGAGTLNISGFAVKNFGTFVRSCGNCSTQY-RRTINLNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPILELAPGAVLKNVIIGAPAADGVHCKG----SCTLQNVWWEDVGEDAATFRGSSSSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative
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            bromodomain; 2Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27499 MW;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 239; DB 2;
Pred. No. 1.1e-07;
5; Mismatches 74
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                                                                                                                                                                  Smolik S.M.,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                  Q9ZU23 PRELIMINARY;
Q9ZU23;
01-MAY-1999 (TTEMBLTel. 1
01-MAY-1999 (TTEMBLTEL. 1
01-MAY-2000 (TTEMBLTEL. 1
                                                                                         Li J., Kremenetskaia I., Luros J., Gonzalez A., Altafi H. Buehler E., Conway A.B., Conn L., Dunn P., Hansen N., Hu Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thallana chromosome 1 BAC F5F19 sequence.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006216; AAD12691.1;
                                                                                                                                                                                        SEQUENCE FROM N.A. Vysotskaia V.S., S. Li J., Kremenetska
                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02172; KIX; 1.
PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN_1;
PROSITE; PS50014; BROMODOMAIN_2;
SMART; SM00291; ZnF_Zz; 1.
SEQUENCE 3190 AA; 331879 MW;
              InterPro; IPR001229; -.
Pfam; PF01419; Jacalin; 3.
PROSITE; PS00225; CRYSTALL
                                                                            EMBL; AC006216; AAI
HSSP; P18670; 1JAC
                                                                                                                                                                                                                                                                                                                                       F5F19.6.
                                                                                                                                                                                                                                                                                                                                                    F5F19.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1623 EAMDVDEAGGSTAGEH----HGEGGGGSGVGGGKDNINGAHDGGATGGAVDIKPKTETK 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1305 TPTSLEALNAGAGAPGTGGSASNVTVSAPSPSPGFLSNGP----SIGTP----SNNNNSS
                                                             InterPro; IPR001064; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 QEVTIDNVHAQNVGEDLITVKGEGGAAV----TNLNIKNSSAKGADDKVVQLNANTHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TPLDFSALSGKSPQPNTFGEQN--TQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 KPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGL----GTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARDNDDETPSPSGENTNGSGGSGN----AGGMASKGKLDSIKQDDDIK------K 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFMDDSCGGNNDSSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFTADKSMGNGDQGENQKPMFELAEGATLKNVN------LGENEVDGIHVKAKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AGGGSSTTPASNPLLLMSGGTAGGGTGATTTTSTSSSSRMMSSSSSLSSQMAALEAA 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTATGGGSGGTPTA-----TGGGEGGVTPQIT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SADSGGGGTPDATGGGGGDTPSATGGGGGG-----DTPTA----TGGGGSGGGGT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCASSGSGSNSSSGATAAGASSTSSSSSAGSGTPLSSVSTPTSATMATSSGGGGGGGGU
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 ΑĄ;
                                                                                                                                                                                                          Schwartz J.R.,
CRYSTALLIN_BETAGAMMA; UNKNOWN_1.; 73939 MW; E4323AF993B1D95E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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Pred. No. 5.2e
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                        Toriumi M., Yu G., Lenz C., Liu S
J., Gonzalez A., Altafi H., Araujo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
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                                                                                                                                                                           Hansen N., Huizar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                             Davis
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Query Match

Local

Similarity

9.8%;

Score 215; DB 10; Pred. No. 1.1e-05;

Length 730;

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RESULT 11
Q9W321
ID Q9W321
DT 01-MAX
RO ENEATY
OC ENEATY
OC Pteryg
OC EDHYGI
RN (1)
RN
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RX MEDLINE-20196006; PubMed=10731132;

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Barlew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M.,

RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Dodson K.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W321;
Q9W321;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGNGGNQWDD-GTDHDGVMKIH------VAVGGLGIEQIRFDYVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGLGT-PSADSGGGGTPDATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGT---PDSTVQNPQDA--SKPNDSQSN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTNGGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3275
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RESULT Q00843 ID Q0 AC Q0 DT 01 DT 01

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., PacLeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri v., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
DR EMBL, AE003448, AAF46516.1; -.
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Best Local Similarity
Matches 105; Conserv
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                                                                                                                                                                                                                                        1466
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  1622
                                                                                                                                                                                                                                                                                                                    1406
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PROSITE; PS50014; BROMODOMAIN_2;
SMART; SM00297; BROMODOMS
SEQUENCE 3275 AA; 340672 MW;
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InterPro; IPR000197; -.
InterPro; IPR000433; -.
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InterPro; IPR003101; -
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                                    294 QEVTIDNVHAQNVGEDLITVKGEGGAAV----TNLNIKNSSAKGADDKVVQLNANTHLK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TPLDFSALSGKSPQPNTFGEQN--TQQAIDPSALLFGSDTQKDVNFGTPDSTVQNPQDAS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X., Mattei B., McIntosh T.C., McLeod M.P.,
EAMDYDEAGGSTAGEH----HGEGGGGSGVGGGKDNINGAHDGGATGGAVDIKPKTETK
                                                                              EFMDDSCGGNNDSSQ----MDCSTGGGKGKNVNNDGTSMIKMEIKTEDGLDG-EVKIK-T
                                                                                                                   TFTADKSMGNGDQGENQKPMFELAEGATLKNVN------LGENEVDGIHVKAKNA 293
                                                                                                                                                          ARDNDDETPSPSGENTNGSGGSGN----AGGMASKGKLDSIKQDDDIK-----K 1567
                                                                                                                                                                                ---AGGGSSTTPASNPLLLMSGGTAGGGTGATTTTSTSSSSRMMSSSSSLSSQMAALEAA 1522
                                                                                                                                                                                                                                                                             PTATGGGSGGTPTA-----TGGGEGGVTPQIT-----
                                                                                                                                                                                                                                                                                                                  ATCASSGSGSNSSSGATAAGASSTSSSSSAGSGTPLSSVSTPTSATMATSSGGGGGGGGG 1465
                                                                                                                                                                                                                                                                                                                                                       ----SADSGGGGTPDATGGGGGDTPSATGGGGGG------DTPTA-----TGGGGSGGGGT 169
                                                                                                                                                                                                                                                                                                                                                                                              SANNNPPSVSSLMQ------QPLSN---RPGTPPYIPASPVPATSASGLAASSTPASAA 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                   KPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGGL---GTP---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPTSLEALNAGAGAPGTGGSASNVTVSAPSPSPGFLSNGP----SIGTPSNNNNN----S
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AA; 3
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25.1%;
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Pred. No. 7.
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Best Local Similarity
Matches 109; Conser
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P93658;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napus (Rape).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                            EMBL; Y11483; CAA72271.1;
HSSP; P18670; 1JAC.
                                                                                                                                                                                                                                                                                                                                                          Geshi N., Brandt A.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GLOBAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                             119
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                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                      Mendel; 14859; Brana;2387;14859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nectria haematococca mpVI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GGEGGVTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVGAGEVFDGHGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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Y--DRGSGACKGQNEGGDKDAVFLLHEGATLKNVIIGKDQSEGVHCKG----HCTLEFVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYTGGV-PKPTDHISN-----
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PF01419; Jacalin; 4.
NCE 680 AA; 69937
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                                                                              Conservative
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                                                                                                      9.3%;
22.7%;
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                                                                                                                                                                                                             MW.
                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 208; DB 3; Le
Pred. No. 6.7e-06;
Pred. No. 57;
                                                                         Score 204.5; DB 10
Pred. No. 4.3e-05;
3; Mismatches 139;
                                                                                                                                                                                                        8CD0CF16C30CA1E2 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB0B8EE72B3B0FB5 CRC64
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                                                                                                                               DB 10;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96400363; PubMed=8806739;
Guo W., Gonzalez-Candelas L., Kolattukudy P.E.;
"Identification of a novel pelD gene expressed uniquely in planta
Fusarium solani f. sp. pisi (Nectria haematococca, mating type VI)
characterization of its protein product as an endo-pectate lyase."
Arch. Biochem. Biophys. 332:305-312(1996).
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezi
Hypocreales; Nectriaceae; Nectria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nectria haematococca mpVI.
                                                                                                                                                                                                                                                                   175 GGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVSDTAGSTEQAGKINVVKDTIKVG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 QTYDGIGAVKFVYNKGSSEIIGDEHGKSTLLGFEEFELNYPSEYI--TEVHGTYDKISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
                            295 EVTIDNYHAQNYGEDLITYKGEGGAAVTNLNIKNSSAKGADDKVYQLNANTHLKIDNFKA 354
                                                                                                                                                          235 AGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNVNLGENEVDGIHVKAKNAQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
99
                                                                                                                                                                                                                   21 GYTGGVPKATG-----SKSLSAPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFHGRAGATISAIGVYLAPVGTIPLTPATQTKKLEAKGGDGGTTWDDGAFDGIRKVSVG
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SCNIEFAWFEDVCEDAISILGSGTA----NIIGGGAYHASDKVIQHNGCGHVNIVNFYA 153
                                                                                                      KGEVFDAGWVRYDRGVKCSGQAEGGSKDAVFILEEGATLRNVIIGANQREGIHCKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LNGIEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGESGAVWDDGAHDNVKKVSVGQ-----GTDGIAAVKFEYRNGSSVVIGAERGTPTLLG
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                                                                                                                                                                                                                                                                                                                         Similarity
72; Conserv
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Grembled.
Grembled.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24509 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQAS
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                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                             Score 203.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2FF53A0D9A4E2CB9
                                                                                                                                                                                                                                                                                                                            Mismatches
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1.4e-05;
78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Length
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RESULT 15
Q21835
ID Q21835
AC Q21835
AC Q21835
AC Q21835
OT 01-NOV
DT 01-NOV
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; Z68008; CAA92000.1; -.
InterPro; IPR001767; -.
InterPro; IPR001990; -.
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Pseudomonas syringae p
transcriptional units
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Keen, N.T.
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Lorang, J.M. and Keen, N.T.
Characterization of avrE from Pseudomonas syringae
hrp-linked avirulence locus consisting of at least
transcriptional units
                                                                                                                                                                                                                                                                                                                                                                                                        pseudomonas syringae pv. t
pseudomonas syringae pv. t
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                      Submitted (18-OCT-1994) Noel T. Keen, Plant Pathology, of California at Riverside, Riverside, CA 92521, USA
                                                                                                                                                                                                                                                                                          Direct
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                                          Conservative
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                                                                                                  /Protein_id="AAC33432.1"
/db_xref="GI:563241"
/translation="MPLTSSKLNPKHPHPYRTDSDTATCSGKPWSWRRSNCPLSEVTQ
HEHRHTPAATDHHAAREFGAKRQESSTKHVRRAEHSASDRPECTVVRQRHTERRQLR
HARGHRPESAGROQAOROPVQHR"
HARGHRPESAGROQAOROPVQHR"
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/db_xref="taxon:323"
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/product="unknown"
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Erwinia amylovora
  Direct Submission
Submitters
                                  Kim,J.F. and Beer,S.V.
HrpW of Erwinia amylovora, a new harpin that contains homologous to pectate lyases of a distinct class J. Bacteriol. 180 (19), 5203-5210 (1998)
                                                                                1 (bases 912 to 2255)
Kim,J.F., Zumoff,C.H. and Beer,S.V.
HrpW, a new harpin of Erwinia amylopectate lyases
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Erwinia amylovora.
Erwinia amylovora
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                                                                Phytopathology 87, S52
2 (bases 1 to 2708)
                                                                                                                                                  type III protein secretion;
Submitted (18-MAR-1997)
                             98422475
                                                                                                              Erwinia
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                     (bases 1 to 2708)
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Plant Pathology, Cornell University,
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